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OM nucleic - nucleic search, using sw model

Run on: February 10, 2005, 06:08:13 ; Search time 370 Seconds
(without alignments)

Title: US-10-647-089-93

Perfect score: 321

Sequence: 1 ttgaccacaaatgcactaa.....acgaaacctcgacaaacag 321

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:
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 19: /cgn2_6/podata/2/pubpna/us11 NEW_PUB.BEQ:/*
 20: /cgn2_6/podata/2/pubpna/us60_NEW_PUB.BEQ:/*
 21: /cgn2_6/podata/2/pubpna/us60_PUBCOMB.seq:/*

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 Sequence 7392, Ap
 c 14 42.8 13.3 10232 15 US-10-282-122A-5487
 Sequence 5487, Ap
 c 15 42 13.1 1959 15 US-10-156-761-4513
 Sequence 4513, Ap
 c 16 42 13.1 9025608 15 US-10-156-761-1
 Sequence 1, Appl
 c 17 41.6 13.0 996 16 US-10-282-122A-11268
 Sequence 11268, A
 c 18 41.2 12.8 936 17 US-10-437-963-76527
 Sequence 76527, A
 c 19 41 12.8 400 9 US-09-867-701-4968
 Sequence 4968, Ap
 c 20 40.8 12.7 1232 17 US-10-437-963-79422
 Sequence 79422, A
 c 21 40.6 12.6 2580 15 US-10-156-761-3895
 Sequence 3895, Ap
 c 22 40.6 12.6 3044 17 US-10-437-963-79637
 Sequence 79637, A
 c 23 40.4 12.6 954 16 US-09-712-363-39
 Sequence 363, Ap
 c 24 40.4 12.6 954 16 US-10-282-122A-28300
 Sequence 2830, A
 c 25 40.4 12.6 45191 15 US-10-080-170-64
 Sequence 64, App
 c 26 40.4 12.6 45191 17 US-10-080-170-64
 Sequence 64, App
 c 27 40.4 12.6 45191 18 US-10-468-356-64
 Sequence 649, App
 c 28 40.4 12.6 45191 18 US-10-468-356-64
 Sequence 649, App
 c 29 40.2 12.5 307 18 US-10-425-115-11105
 Sequence 11105, Ap
 c 30 40.2 12.5 1803 15 US-10-156-761-4657
 Sequence 4657, Ap
 c 31 40.2 12.5 1824 17 US-10-767-701-13070
 Sequence 13070, A
 c 32 39.8 12.4 1300 17 US-10-437-963-22867
 Sequence 22867, A
 c 33 39.6 12.4 1318 16 US-10-425-114-14884
 Sequence 14884, A
 c 34 39.6 12.3 1446 15 US-10-156-761-4324
 Sequence 4324, Ap
 c 35 39.6 12.3 1460 16 US-10-425-114-14893
 Sequence 14893, A
 c 36 39.6 12.3 1512 13 US-10-12-800-31
 Sequence 31, Appl
 c 37 39.6 12.3 1512 18 US-10-810-352-31
 Sequence 352, A
 c 38 39.6 12.3 2073 16 US-10-425-114-29125
 Sequence 29125, A
 c 39 39.6 12.3 4509 13 US-10-12-800-5
 Sequence 5, Appl
 c 40 39.6 12.3 4509 18 US-10-810-352-5
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 c 41 39.6 12.3 4512 13 US-10-124-100-27
 Sequence 27, Appl
 c 42 39.6 12.3 4512 18 US-10-810-352-27
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 c 43 39.6 12.3 4767 15 US-10-331-061-76
 Sequence 76, Appl
 c 44 39.4 12.3 394 16 US-09-815-24-7862
 Sequence 7862, Ap
 c 45 39.4 12.3 1488 16 US-10-282-122A-30375
 Sequence 30375, A

RESULT 1 09-894-844-93

; Sequence 93, Application US/09894844
 ; Patent No. US20020176673A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Behr, Marcel
 ; APPLICANT: Small, Peter
 ; APPLICANT: Schoolnik, Gary
 ; APPLICANT: Wilson, Michael A.
 ; TITLE OF INVENTION: Molecular Differences Between Species of
 ; TITLE OF INVENTION: the M. Tuberculosis Complex
 ; FILE REFERENCE: STAN102CON
 ; CURRENT APPLICATION NUMBER: US/09/894,844
 ; CURRENT FILING DATE: 2001-06-27
 ; PRIORITY APPLICATION NUMBER: 09/318,191
 ; PRIORITY FILING DATE: 1999-05-25
 ; PRIORITY APPLICATION NUMBER: 60/097,936
 ; PRIORITY FILING DATE: 1998-08-25
 ; NUMBER OF SEQ ID NOS: 137
 ; SOFTWARE: FastS9Q for Windows Version 4.0
 ; SEQ ID NO: 93
 ; LENGTH: 321

; TYPE: DNA
 ; ORGANISM: Mycobacteria tuberculosis
 US-09-894-844-93
 Query Match 100.0%; Score 321; DB 9; Length 321;
 Best Local Similarity 100.0%; Pred. No. 9.3e-90;
 Matches 321; Conserv 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TTGACCCACAGCGACTAACGGCCATACGGCCGCCAGGCTCACGCCCGCT 60
 1 TTGACCCACAGCGACTAACGGCCATACGGCCGCCAGGCTCACGCCCGCT 60

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	321 100.0	321 9	US-09-894-844-93	Sequence 93, Appl	
2	321 100.0	321 16	US-10-388-902-93	Sequence 93, Appl	
3	321 100.0	321 16	US-10-647-089-93	Sequence 93, Appl	
c 4	44.8	14.0 1599	15 US-10-156-761-2897	Sequence 2897, Appl	
5	44.8	14.0 9025608	15 US-10-156-761-1	Sequence 1, Appl	
6	44 13.7	909 18	US-10-425-115-73640	Sequence 73640, A	
7	43.8	13.6 3480	15 US-10-369-493-39466	Sequence 39466, A	
8	43.8	13.6 3480	15 US-10-369-493-39849	Sequence 39849, A	
9	43.8	13.6 3501	15 US-10-369-493-39098	Sequence 39098, A	
10	43	13.4 1193	16 US-10-425-114-24011	Sequence 24011, A	
11	43	13.4 1308	16 US-10-425-115-9576	Sequence 49576, A	
c 12	42.8	13.3 4200	9 US-09-815-242-4124	Sequence 4124, Ap	

RESULT 3
Db 61 CGGAATCGGTTGGCCGAAACATGGTCCCAGCAGTCAGGTATGCCAGATGGGG 120
Qy 121 CGGCCCAAGCGGAGCTCTGGCTGGAGATGGGG 180
Db 121 CGGCCCAAGCGGAGCTCTGGCTGGAGATGGGG 180
Qy 181 ACATCACCGAAATGACGAGGAGAACAGGGAACTGGCTGATCTGCAC 240
Db 181 ACATCACCGAAATGACGAGGAGAACAGGGAACTGGCTGATCTGCAC 240
Qy 241 GATGAGCAAGGGCTTAGGGGGATGAAGCTGGCTGGCATCCATCCC 300
Db 241 GATGAGCAAGGGCTTAGGGGGATGAAGCTGGCTGGCATCCATCCC 300
Qy 301 GACGAACCCGACAGGAAACAG 321
Db 301 GACGAACCCGACAGGAAACAG 321

RESULT 2
US-10-388-902-93
; Sequence 93, Application US/10388902
; Publication No. US20040016574A1
GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; CURRENT APPLICATION NUMBER: STAN102CON
; CURRENT FILING DATE: 2003-08-21
; PRIORITY NUMBER: US/09/894,844
; PRIORITY FILING DATE: 2001-06-27
; PRIORITY APPLICATION NUMBER: US/09/181,191
; PRIORITY FILING DATE: 1999-05-25
; PRIORITY APPLICATION NUMBER: 60/097,936
; PRIORITY FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 93
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-10-647-089-93

Query Match 100 %; Score 321; DB 16; Length 321;
Best Local Similarity 100 %; Pred. No. 9.3e-90; Indels 0; Gaps 0;
Matches 321; Conservative 0; Mismatches 0;

Qy 1 TTGACCCACAAGGCACATAACGCCAGCCATGCCAGGGCTAACGCCGCT 60
Db 1 TTGACCCACAAGGCACATAACGCCAGCCATGCCAGGGCTAACGCCGCT 60
Qy 61 CGGAATGGTTGGGGCAATGGTTGGCCGCCGACGTTCCGTCGCGAGCGC 120
Db 61 CGGAATGGTTGGGGCAATGGTTGGCCGCCGACGTTCCGTCGCGAGCGC 120
Qy 121 CGCGCCAAACGCCAGGGACTCTGGCTATCCGGAGATACTGGTGCG 180
Db 121 CGGCCAAACGCCAGGGACTCTGGCTATCCGGAGATACTGGTGCG 180
Qy 181 ACATCACCGAAATGACGAGGAGAACAGGGAACTGGCTGGCTGGCTGAC 240
Db 181 ACATCACCGAAATGACGAGGAGAACAGGGAACTGGCTGGCTGAC 240
Qy 241 GATGAGCAAGGGCTTAGGGGGATGAAGCTGGCTGGCATCCATCCC 300
Db 241 GATGAGCAAGGGCTTAGGGGGATGAAGCTGGCTGGCATCCATCCC 300
Qy 301 GACGAACCCGACAGGAAACAG 321
Db 301 GACGAACCCGACAGGAAACAG 321

RESULT 4
US-10-156-761-2997/c
; Sequence 2997, Application US/10156761
; Publication No. US20030119018A1
GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAMI, YOSHITUKI
; APPLICANT: HATTORI, MASAHIRA

Qy 181 ACATCACCGAAATGACGAGGAGAACAGGGAACTGGCTGGCTGGCTGAC 240
Db 181 ACATCACCGAAATGACGAGGAGAACAGGGAACTGGCTGGCTGGCTGAC 240
Qy 241 GATGAGCAAGGGCTTAGGGGGATGAAGCTGGCTGGCATCCATCCC 300
Db 241 GATGAGCAAGGGCTTAGGGGGATGAAGCTGGCTGGCATCCATCCC 300
Qy 301 GACGAACCCGACAGGAAACAG 321

Page 3

1 / TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 2 / FILE REFERENCE: 249-262
 3 / CURRENT APPLICATION NUMBER: US/1.0/155,761
 4 / CURRENT FILING DATE: 2002-05-29
 5 / PRIORITY APPLICATION NUMBER: JP 2001-204089
 6 / PRIOR FILING DATE: 2001-05-30
 7 / PRIORITY APPLICATION NUMBER: JP 2001-227697
 8 / PRIOR FILING DATE: 2001-08-02
 9 / NUMBER OF SEQ ID NOS: 15109
 10 / SEQ ID NO: 2997
 11 / LENGTH: 1599
 12 / TYPE: DNA
 13 / ORGANISM: Streptomyces avermitilis
 14 / FEATURE: CDS
 15 / NAME/KEY: CDS
 16 / LOCATION: (1)..(1599)
 17 / US-10-156-761-2997

18 / Query Match Score 44.8; DB 15; Length 1599;
 19 / Best Local Similarity 51.5%; Pred. No. 0.0051; Indels 0; Gaps 0;
 20 / Matches 103; Conservative 97; Mismatches 97;

21 / Qy 42 AGGGCTAACGCCCGCCGGTGGAAATCCGTTGGCGCAAACATGGTTGGCCGGCAGCT 101
 22 / Db 415 AGGGCGGCCAACCGCGCGCACCGCGCGTGGCCGGACCCGGTCCGGCGGACCA 356
 23 / Qy 102 TCCGTGGCGAGCAGGGACATCACAGGAACCGGCTATCGCGGAC 161
 24 / Db 355 CGCGCGGAGCACCGCGGGCGGCGGAGCGGAGCATCGCGGCC 296
 25 / Qy 162 GTACGGCGAGTGGGACATCACAGGAACCGGACTCGCGGCT 221
 26 / Db 295 AGCCCAAGCAGGGTGGCGGAGGGAGTACCGATGGACAGCGGCC 236
 27 / Qy 222 GTTGTGCGATGCACTTCGAG 241
 28 / Db 235 GTTGCAGCGGCAAGATCGAGG 216

29 / RESULT 5
 30 / US-10-156-761-1
 31 / Sequence 1, Application US/10156761
 32 / Publication No. US20030119018A1
 33 / GENERAL INFORMATION:
 34 / APPLICANT: OMURA, SATOSHI
 35 / APPLICANT: IKEDA, HARUO
 36 / APPLICANT: ISHIKAWA, JUN
 37 / APPLICANT: HORIKAWA, HIROSHI
 38 / APPLICANT: SHIBA, TADAYOSHI
 39 / APPLICANT: SAKAKI, YOSHIIYUKI
 40 / APPLICANT: HATTORI, MASAHISA
 41 / TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 42 / FILE REFERENCE: 249-262
 43 / CURRENT FILING DATE: 2002-05-29
 44 / PRIOR APPLICATION NUMBER: US/10/156,761
 45 / PRIOR FILING DATE: 2001-05-30
 46 / PRIOR APPLICATION NUMBER: JP 2001-204089
 47 / PRIOR FILING DATE: 2001-08-02
 48 / NUMBER OF SEQ ID NOS: 15109
 49 / SEQ ID NO: 1
 50 / LENGTH: 9025608
 51 / TYPE: DNA
 52 / ORGANISM: Streptomyces avermitilis
 53 / FEATURE: misc feature
 54 / LOCATION: (4187715)
 55 / OTHER INFORMATION: a, t, c, g, other or unknown
 56 / US-10-156-761-1

57 / RESULT 6
 58 / US-10-425-115-73640
 59 / Sequence 73640, Application US/10425115
 60 / Publication No. US200401427A1
 61 / GENERAL INFORMATION:
 62 / APPLICANT: La Rosa, Thomas J.
 63 / APPLICANT: Kovacic, David K.
 64 / APPLICANT: Zhou, Yuhua
 65 / APPLICANT: Cao, Yongwei
 66 / TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 67 / FILE REFERENCE: 38-21 (53222) B
 68 / CURRENT APPLICATION NUMBER: US/10/425,115
 69 / CURRENT FILING DATE: 2003-04-28
 70 / NUMBER OF SEQ ID NOS: 369326
 71 / SEQ ID NO: 73640
 72 / LENGTH: 909
 73 / TYPE: DNA
 74 / ORGANISM: Zea mays
 75 / FEATURE:
 76 / OTHER INFORMATION: Clone ID: MRT4577_167159C.1
 77 / US-10-425-115-73640

78 / RESULT 7
 79 / US-10-169-493-39466
 80 / Sequence 39466, Application US/10369493
 81 / Publication No. US20030233675A1
 82 / GENERAL INFORMATION:
 83 / APPLICANT: Cao, Yongwei
 84 / APPLICANT: Hinkle, Gregory J.
 85 / APPLICANT: Slater, Steven C.
 86 / APPLICANT: Goldman, Barry S.
 87 / APPLICANT: Chen, Xianfeng
 88 / TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 89 / FILE REFERENCE: 38-10 (52052) B
 90 / CURRENT APPLICATION NUMBER: US/10/369,493
 91 / CURRENT FILING DATE: 2003-02-28
 92 / US-10-156-761-1

PRIOR APPLICATION NUMBER: US 60/360, 039
 PRIOR FILING DATE: 2002-07-21
 SEQ ID NO: 39466
 LENGTH: 3480
 TYPE: DNA
 ORGANISM: Xanthomonas campestris
 US-10-369-493-39466

Query Match 13.6%; Score 43.8; DB 15; Length 3480;
 Best Local Similarity 55.6%; Pred. No. 0.0011;
 Matches 84; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy 111 CGAGCAGGCCCAACGGCACCTCGAGGTATCGCCGAGCTACGCCGA 170
 Db 924 CCAGCACCGCCGAACTCGAACAGCGGACTCTCGATCGCTGCAAGGAGCGCA 983

Qy 171 GATGGGGGACATCACAGGAATTGACCAGACAGCGGAACCTGGGCTTGTGAT 230
 Db 984 GCTGAGGGAGCTCACCCAGACATAGCGCAGACTCCGCAGTAAGCTGGGTTGTGCGGA 1043

Qy 231 GCATCTGGGATGGACGGGCGGGCTTGAG 261
 Db 1044 GGCAGTCGGGATGCCGAACCGCAAGCTGGAG 1074

RESULT 8
 US-10-369-493-39849
 Sequence 39849, Application US/10369493
 Publication No. US20030233675A1

GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 FILE REFERENCE: 38-0-(52052)B

CURRENT APPLICATION NUMBER: US 10/369, 493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360, 039
 PRIOR FILING DATE: 2002-07-21
 SEQ ID NO: 39849
 LENGTH: 3480
 TYPE: DNA
 ORGANISM: Xanthomonas campestris
 US-10-369-493-39849

Query Match 13.6%; Score 43.8; DB 15; Length 3480;
 Best Local Similarity 55.6%; Pred. No. 0.0011;
 Matches 84; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy 111 CGAGCAGGCCCAACGGCACCTCGAGGTATCGCCGAGCTACGCCGA 170
 Db 924 CCAGCACCGCCGAACTCGAACAGCGGACTCCGCAGTAAGCTGGGTTGTGCGGA 983

Qy 171 GATGGGGACATCACAGGAATTGACCAGACAGCGGAACCTGGGCTTGTGAT 230
 Db 984 GCTGAGGGAGCTCACCCAGACATAGCGCAGACTCCGCAGTAAGCTGGGTTGTGCGGA 1043

Qy 231 GCATCTGGGATGGACGGGCGGGCTTGAG 261
 Db 1044 GGCAGTCGGGATGCCGAACCGCAAGCTGGAG 1074

RESULT 9
 US-10-369-493-39098
 Sequence 39098, Application US/10369493
 Publication No. US20030233675A1

GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(5331)B

CURRENT APPLICATION NUMBER: US 10/425, 114
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO: 39098

Query Match 13.4%; Score 43; DB 16; Length 1193;
 Best Local Similarity 50.2%; Pred. No. 0.0018;
 Matches 106; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

Qy 107 CGGCCAGCAGGCCGCCAACGGCACCTCGAGGTATCGCCGAGCTACGCCGA 166
 Db 331 CGCGGGAGGAGCTACCCAGACTCCGCAGTAAGCTGGGTTGTGCGGA 390

Qy 167 CGGAGATGGCGCATCACAGAATCGAACAGCGGAACCTGGGCTTGTGCGT 226
 Db 391 CGGGCGCTGGAGGGCGGGCTCCGGCGACGGCTGGCGTGAAGCTGGGG 450

Qy 227 CGATGGATCTCGAGATGAGCAGCCGGCTTGAGGAGGGATGAAGCTGGCTGGCATC 286

RESULT 11
 US-10-425-115-49576
 ; Sequence 49576, Application US/10425115
 ; Publication No. US20040214772A1
 GENERAL INFORMATION:
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 369326
 SEQ ID NO 49576
 LENGTH: 1308
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE:
 OTHER INFORMATION: Clone ID: MRT4577_145214C.1
 US-10-425-115-49576

Query Match 13.4%; Score 43; DB 18; Length 1308;
 Best Local Similarity 50.2%; Pred. No. 0.0016;
 Matches 105; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

Qy 107 CGGCCAGCACGGCCGACCTCGGACTTCGGAATCCGGCTGAGCTTGCATC 166
 Db 331 CGCGGAGATAAACCTGTCCCTGCCGGGGCGCCAGG 390

Qy 167 CGAGATGGTGAGCATCACAGAAATCGAGACAGCGAACTGGGCTGTGT 226
 Db 391 CGGGGTGGAGCGGGGTGCGCTGGCTGGCGAGGGCTAGG 450

Qy 227 CGATGATCTGACGTGAGGAAGCGGGGATGAAGCTCGCTGACATC 286
 Db 451 CGCGGACCTGTGGCGCCCTGGGGGGGGCTCCCTCGCTGGCGCG 510

Qy 287 CGTATCCTTCCCGAGAACGGACAGCA 317
 Db 511 ACTCCGGCTCCGAGGGGAGCTGCA 541

RESULT 12
 US-09-815-242-4124/c
 ; Sequence 4124, Application US/09015242
 ; Patent No. US2002006159A1
 GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes
 FILE REFERENCE: ELITRA.011A
 CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIORITY DATE: 2000-03-21
 PRIORITY APPLICATION NUMBER: 60/206,848

RESULT 13
 US-10-282-122A-7392/C
 ; Sequence 7392, Application US/10282122A
 ; Publication No. US20040029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,315
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR APPLICATION NUMBER: 60/253, 625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257, 931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267, 636
 ; PRIOR FILING DATE: 2000-12-09
 ; PRIOR APPLICATION NUMBER: 60/267, 636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269, 308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PAM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 78614
 ; LENGTH: 4200
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium avium
 ; US-10-282-122A-25487

Query Match 13.3%; Score 42.8; DB 16; Length 10232;
 Best Local Similarity 47.7%; Pred. No. 0; 0.002%;
 Matches 125; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

Qy 20 AACGCAGCCACGGCATTCGCCAGGGCTAACGCCCGCGCTGGATCGCTGGCGGC 79
 Db 1271 AACGTGAGCCGGAGGCGCTGGATGACCGTGGCTGGCGCTGA 1330

Qy 80 AACATGGTTGGCGGGGACACTGGCGGCGACAGCGCCAAAGGCACGGCG 139
 Db 1331 CGGAGCCGCACCCCGCGTGATCCCGAACCGACGCA 1390

Qy 140 ACCTCAGGGTATCCGCCGAGCGTAGCCGGATGGTGGCACATCACGAAATTGACG 199
 Db 1391 CCCCCGAGCGCTGGCGATGCGTGGGGACCTCGTGTGACCGTGGCGACG 1450

Qy 200 AGCACAGCCAACTGGCGTGGTGTGATGATCATCTGAGATGAGCTGGCTTGG 259
 Db 1451 AGGGTGTCAACGGCTGGCCATCTCGCGACCCGGCGAGCTGGCTGG 1510

Qy 260 AGGGGGATGAAGCTGGCTG 281.
 Db 1511 TGGCGTGTGATGTCCCCTGG 1512

RESULT 14
 US-10-282-122A-25487
 Sequence 25487, Application US/10282122A
 Publication No. US20040029129A1.
 GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangshu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cherry L
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlson, Kari
 ; APPLICANT: Zykind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELTRIA 034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27

; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 25487
 ; LENGTH: 10232
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium avium
 ; US-10-282-122A-25487

Query Match 13.1%; Score 42; DB 15; Length 1959;
 Best Local Similarity 50.5%; Pred. No. 0.0038%;
 Matches 102; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

RESULT 15
 US-10-156-761-4513
 Sequence 4513, Application US/10156761.
 Publication No. US2003119018A1.
 GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIOKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO: 4513
 ; LENGTH: 1959
 ; TYPE: DNA
 ; ORGANISM: Streptomyces avermitilis
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1) .. (1959)

; US-10-156-761-4513

Qy 20 AACGCCAGCCAGCCATGGCCAGGGCTAACGCCCGTCGGAAATCGCGTGGGC 79
Db 365 AGCACACACCTCAACGTCACCGAACCTGGCGACTGGCGACCTGGCCCGTGGGGCC 424
Qy 80 AACATGGTTGGCGGCCAACCTCCCTCGCGAGCGAGCGGCCAACGGGAAGCGG 139
Db 425 GGCACGGACCCGACCCGAACTGGCCGCCCCCTCCCGCGACCGCCCGCCCG 484
Qy 140 ACCTCGAGGTATCCCGAGGTAGCCCGAGATGGTGCCGAACTACAGAAATGACCG 199
Db 485 TCGAGACGAGCCCGAGCATGACCAACCGCATCTGGCGGACCGAGTTCGACC 544
Qy 200 ACGACACAGCGGAACCTGGCGT 221
Db 545 CGTGGTTCGGGACCTGGTGGT 566

Search completed: February 10, 2005, 07:36:14
Job time : 390 secs



Copyright GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 10, 2005, 05:25:02 ; Search time 75 Seconds
(without alignments)
3042.176 Million cell updates/sec

Title: US-10-647-089-93
Perfect score: 321
Sequence: 1 ttgaccacaaggcactaa.....acgaaccggacagcaaacag 321

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 4 summaries

Database : Issued_Patents_NA.*

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3: /cgnd_6/picodea/1/ina/A_-COMB .seq;*
4: /cgnd_6/picodea/1/ina/6B_-COMB .seq;*
5: /cgnd_6/picodea/1/ina/PCNTS COMB .seq;*
6: /cgnd_6/picodea/1/ina/backfile1.seq;*

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	321	100.0	321	4	US-09-894-84-93	
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c	321	100.0	4411529	3	US-09-103-84-0A-2	
c	42.8	13.3	4212	4	US-09-252-991A-4748	
c	42.8	13.3	4242	4	US-09-252-991A-4697	
c	40.4	12.6	4433765	3	US-09-103-84-0A-2	
c	40.4	12.6	4411529	3	US-09-103-84-0A-1	
c	40.2	12.5	732	4	US-09-252-991A-6298	
c	9	40.2	12.3	945	4	US-09-232-991A-6167
c	10	40.2	12.5	1602	4	US-09-252-991A-6382
c	11	39.8	12.4	594	4	US-09-232-991A-12043
c	12	39.8	12.4	966	4	US-09-232-991A-11896
c	13	39.8	12.4	1179	4	US-09-252-991A-12017
c	14	39.6	12.3	4767	4	US-09-231-899-76
c	15	39.4	12.3	1470	4	US-09-232-991A-6325
c	16	39.4	12.3	1473	4	US-09-252-991A-6144
c	17	39.4	12.3	1512	4	US-09-232-991A-6219
c	18	39.2	12.2	1320	4	US-09-724-977-85
c	19	38.8	12.1	408	4	US-09-252-991A-655
c	20	38.8	12.1	801	4	US-09-232-991A-698
c	21	38.8	12.1	1356	4	US-09-232-991A-630
c	22	38.8	12.1	2955	4	US-09-252-991A-684
c	23	38.8	12.1	3150	4	US-09-232-991A-727
c	24	38.4	12.0	1371	4	US-09-232-991A-13554
c	25	38.4	12.0	2181	4	US-09-252-991A-13742
c	26	38.4	12.0	2277	4	US-09-235-991A-13403
c	27	38.4	12.0	2519	4	US-09-638-903-1
c	28	38.4	12.0	2570	4	US-10-140-002-539
c	29	38.2	11.9	888	4	US-09-252-991A-16512
c	30	38.2	11.9	1512	4	US-09-252-991A-16092
c	31	38.2	11.9	2400	4	US-09-252-991A-15991
c	32	37.8	11.8	4257	2	US-08-690-473-1
c	33	37.8	11.8	4257	3	US-09-259-821A-1
c	34	37.8	11.8	4257	3	US-08-843-659-1
c	35	37.8	11.8	4257	4	US-09-825-588A-1
c	36	37.8	11.8	12001	4	US-08-454-568A-1
c	37	37.2	11.6	1488	4	US-09-489-039A-943
c	38	37	11.5	1470	4	US-09-252-991A-896
c	39	37	11.5	1662	4	US-09-252-991A-1137
c	40	37	11.5	1693	3	US-09-320-778-23
c	41	37	11.5	1693	4	US-09-141-908-19
c	42	37	11.5	1693	4	US-09-657-440-23
c	43	37	11.5	1839	4	US-09-252-991A-945
c	44	37	11.5	44377	2	US-08-804-227C-7
c	45	37	11.5	44377	2	US-08-804-198-1

ALIGNMENTS

RESULT 2
US-09-103-840A-2/c
Sequence 2, Application US/09103840A.
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24336-20007.00
CURRENT APPLICATION NUMBER: US/09/103, 840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
"n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 100.0%; Score 321; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 2.4e-74;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 100.0%; Score 321; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 2.4e-74;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OTHER INFORMATION: Mycobacterium tuberculosis

Query 1 TTCACCCACAAGGGCACTAAAGGCCAACCGGATTCGGGAGGGTCAACGCCCGCGT 60
Db 2976906 TTGACCCRACAAGGCACATAAAAGCCATGCCAGCGCATGCCCGCGT 2976847
Query 61 CGGAATCGGTTGGCGCAAATGGGTGGGGCGCAGTCCGTGGCCAGTGGGC 120
Db 2976846 CGGAACTCGGTTGGCGCGCAATGTTGGCCGGCGACGGTCCGGCGACGGC 2976787
Query 61 CGGAACTCGGTTGGCGCGCAATGTTGGCCGGCGACGGTCCGGCGACGGC 180
Db 2976786 CGGGCCRAACGGGAACTGGGCGACCTCGGGGAGCTGGGAGATGGGGCG 2976727
Query 121 CGGGCCRAACGGGAACTGGGCGACCTCGGGGAGCTGGGAGATGGGGCG 180
Db 2976726 ACATCACGGAATTCGAGGAACTGGGCGACCTCGGGGAGCTGGGAGATGGGGCG 2976667
Query 181 ACATCACGGAATTCGAGGAACTGGGCGACATGGGAGCTGGGAGCTGGGAGATTCGAC 240
Db 2976666 GATGAGGAGCGCCGCTTGAGGGGGATGAAGGCTGGCTGGCATCGTACTCCCC 2976607
Query 241 GATGAGGAGCGCCGCTTGAGGGGGATGAAGGCTGGCTGGCATCGTACTCCCC 300
Db 2976606 GATGAGGAGCGCCGCTTGAGGGGGATGAAGGCTGGCTGGCATCGTACTCCCC 2976586

RESULT 4
US-09-252-991A-4748/c
Sequence 4748, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfeld et al.
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.1356
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIORITY FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-01-19
NUMBER OF SEQ ID NOS: 331142
SEQ ID NO 4748
LENGTH: 4212
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4748

Query Match 13.3%; Score 42.8; DB 4; Length 4212;
Best Local Similarity 50.3%; Pred. No. 0.031; Indels 0; Gaps 0;
Matches 104; Conservative 0; Mismatches 102; Mismatches 102;

Query 48 CAACGGCCCGCTGGAAATCGGTTGGCGCCAACTGGTTGGCGCCGACGGTTCGTC 107
Db 1531 CCACGTTCTGGACGAACTGGATGGCTGGCGCTGGCTGGCGCGACGGTTCGTC 1472
Query 108 CGCGAACGAGCGCCGGCTTAAGGGGGATGAACCTCGTGGCATCGTGGCGCTGGCGCGACGGTACGGCTGGCGCTTCAGGGAACTGGCTGGCGCGCTTCAGGGAACTGGTACGGACGG 167
Db 1471 TGGACATCATCGGGCGCGCTTCAGGGAACTGGCTGGCGCGCTTCAGGGAACTGGTACGGACGG 1412

Qy 306 ACCGGACAGAAACAG 321
Db 1129665 GCGGGCAGAAGAACAG 1129680

RESULT 8
US-09-252-991A-6298/c
; Sequence 6298/c
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196-136
; CURRENT FILING DATE: 1999-02-18
; CURRENT FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: US 60/09252, 991A
; PRIOR APPLICATION NUMBER: US 60/074, 788
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 6398
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6298

Query Match Score 40.2 ; DB 4 ; Length 732;
Best Local Similarity 49.3% ; Pred. No. 0.;
Matches 105 ; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

Qy 90 GCGGCCGCGTTCTGGCGAGCAGGCCGACCTCGAGGC 149
Db 692 GCGGATCGCGTGTGGCAACGGCACCCAGGGCAGACCTCGA 633
Qy 150 TATCGGCCAGGTACGCCAGATGGTCCGACATCAGCGAAATTCGAGACACAGC 209
Db 632 TGCGGACCTGGCTTCGGCCAGCGGCCACATCGATGCCCTTGCG 573

Qy 210 CGAACTGGCGTGTGGTCAATCGACGATGGTGGCTTGAGGGGGAT 269
Db 572 CGATCGGCCATTGGCGCCAAAGGCCCTTCGAGCACTTCAGTGACCTCCGGAT 513
Qy 270 GAAGCTGGCTGGATCCSTATCACTTCCCGA 302
Db 512 GGccCTGGAAACAGTCCGATCCCTCGGTGA 480

RESULT 9
US-09-252-991A-6167
; Sequence 6167, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196-136
; CURRENT FILING DATE: 1999-02-18
; CURRENT FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: US 60/094, 190
; PRIOR APPLICATION NUMBER: US 60/09252, 991A
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 6167
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6167

Query Match Score 40.2 ; DB 4 ; Length 945;
Best Local Similarity 49.3% ; Pred. No. 0.;
Matches 105 ; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

Qy 90 GCGGCCGCGTTCTGGCGAGCAGGCCGACCTCGAGGC 149
Db 420 GCGGATCGCGTGTGGTCAACGGCACCCAGGGCAGACCTCGA 479
Qy 150 TATCGGCCAGGTACGCCAGATGGTGGCTTGAGGGGGAT 269
Db 480 TGGCGACTGGCTTCGGCGCCAGGGCAGACCTCGAGGC 539
Qy 210 CGAACTGGCGTGTGGTCAATCGACGATGGCAGGCCCTTGAGGGGGAT 269
Db 540 CGATCGGCCATTGGCGCCAAAGGCCCTTCGAGCACTCCGGAT 599
Qy 270 GAAGCTGGCTGGCATCGTATCACTTCCCGA 302
Db 600 GGGCTCCGGAAACAGTGGATGCGCTCGGTGA 632

RESULT 10
US-09-252-991A-6382/c
; Sequence 6382, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196-136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074, 788
; PRIOR APPLICATION NUMBER: US 60/094, 190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 6382
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6382

Query Match Score 40.2 ; DB 4 ; Length 1602;
Best Local Similarity 49.3% ; Pred. No. 0.;
Matches 105 ; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

Qy 90 GCGGCCGCGTTCTGGCGAGCAGGCCGACCTCGAGGC 149
Db 1222 GCGGATCGCGTGTGGACGGCACCCAGGGCAGACCTCGA 1163
Qy 150 TATCGGCCAGGTACGCCAGATGGTGGCTTGAGGGGGAT 269
Db 1162 TCGGACCTGGCTTCGGCGCCAGGGCCACATCGATGCCCTCGG 1103
Qy 210 CGAACTGGCGTGTGGTCAATCGACGATGGCAGGCCCTTGAGGGGGAT 269
Db 1102 CGATCGGCCATTGGCGCCAAAGGCCCTTCGAGCACTCCGGAT 1043
Qy 270 GAAGCTGGCTGGCATCGTATCACTTCCCGA 302
Db 1042 GGGCTCCGGAAACAGTGGATGCGCTCGGTGA 1010

RESULT 11
US-09-252-991A-12043
; Sequence 12043, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196-136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074, 788

Query Match Score 40.2 ; DB 4 ; Length 945;
Best Local Similarity 49.3% ; Pred. No. 0.;
Matches 105 ; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 12043
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12043

Query Match Score 12.4%; DB 4; Length 594;
Best Local Similarity 53.5%; Pred. No. 0.13;
Matches 83; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
Qy 26 AGCCAGGCCATGCCGAGGGCTCAAGCCCCGGCTGGAAATGCCTTGGCGGAAACATG 85
Db 265 AGGAAGCCATTGCTGGGCGCTGGAAACCCCTGGAACTCTCGGGATCCCT 324
Qy 86 GTTGGCGGGCGACGTTCCGTCCGCGAGGAAGCGCCACAGGGCAGGCGACCTCG 145
Db 325 ACTTCGGAGETGTCGAGGGCCGACCGCGATGAAGGGTCTGGGAAGGGCGCTGGTG 384
Qy 146 AGGCTATCCGGAGGTAACTCGAGATGGTGGCG 180
Db 385 AGGGTTTTCTCGCTGTCCTCGTGAAGTGGCG 419

RESULT 12
US-09-252-991A-11896/c
Sequence 11896, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196_1.136
; CURRENT APPLICATION NUMBER: US/09/252,991A.
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 11896
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11896

Query Match Score 12.4%; DB 4; Length 966;
Best Local Similarity 53.5%; Pred. No. 0.14;
Matches 83; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
Qy 26 AGCCAGGCCATGCCGAGGGCTCAAGCCCCGGCTGGAAATGCCTTGGCGGAAACATG 85
Db 584 AGGAAGCCATTGCTGGGCGCTGGAAACCCCTGGAACTCTCGGGATCCCT 525
Qy 86 GTTGGCGGGCGACGTTCCGTCCGCGAGGAAGCGCCACAGGGCAGGCGACCTCG 145
Db 524 ACTTCGGAGETGTCGAGGGCCGACCGCGATGAAGGGTCTGGGAAGGGCGCTGGTG 465
Qy 146 AGGCTATCCGGAGGTAACTCGAGATGGTGGCG 180
Db 464 AGGGTTTTCTCGCTGTCCTCGTGAAGTGGCG 430

RESULT 13
US-09-252-991A-12017
Sequence 12017, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

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Db 3846 CGGGAGGATACGTTGATGGCCATTGGTGGTGGCTGGCGAGTAGCCCTCGACAGC 3787
Qy 310 GACGCC 315
Db 3786 GATATC 3781

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RESULT 15

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US-09-252-991A-6325
; Sequence 6325, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1995-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 6325
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-6325

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Query Match 12.3%; Score 39.4; DB 4; Length 1470;
Best Local Similarity 54.5%; Pred. No. 0.19;
Matches 79; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
Qy 1 TTGACCCATAAGGCCACTAAAGCCAGCCAGCATCGCCAGGGCTAACGCCCGGT 60
Db 979 TTTCACCGGCGAGATGCCAGGGCCAGCCGGCATCGGCCGCAGCCCTTGACGGT 1038
Qy 61 CGGATTCGCTTGGCGGGACATGGTTGCCGCCGAGTTCGTCGGAGCAGGC 120
Db 1039 CGACAGCAAGGGAGGGAGCTGCGTACCTGGGTCGCCAGTTCGCTTCCTGCG 1098
Qy 121 CGCGCCAAAGGGAGGGACCTCG 145
Db 1099 GGCGCGAACAGGGACAGGGCTCG 1123

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Job time : 96 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 10, 2005, 03:46:41 ; Search time 2098 seconds

Perfect score: 5575.383 Million cell updates/sec

Title: US-10-647-089-93

Sequence: 1 ttgaccacaaggcactaa.....acgaaacctggacagcaacag 321

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Total number of hits satisfying chosen parameters: 65645750

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

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	4: 9b_est3:*
	5: 9b_est4:*
	6: 9b_est5:*
	7: 9b_est6:*
	8: 9b_g981:*
	9: 9b_g982:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	FEATURES	Source
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c 3	46.8		14.6	792	6	CD922090	CD922090 GR45_7.00N		
c 4	45.2		14.1	626	6	CNS0091P	AL053013 Drosophili		
c 5	45.5		14.0	925	9		AL10460 Drosophili		
c 6	44.8		14.0	1101	9	CNS017SY	AL160581 Leishmani AL160634 Leishmani		
c 7	43.6		13.6	532	9	P233L	CB029421 TGEStydy6		
c 8	43.6		13.6	623	9	P230L	BZ2574121 msh2_3520		
c 9	43		13.4	478	6	CB029421	BZ2574121 msh2_3520		
c 10	42.8		13.3	1075	8	BZ574121	BZ2576260 msh2_3520		
c 11	42.8		13.3	1331	8	BZ576260	BZ2574088 msh2_3505		
c 12	42.8		13.3	1348	8	BZ574088	AL067742 Drosophili CA248787 SCSBF110		
c 13	42.6		13.3	932	9	CNS0072Q	CC626073 OGUF33TV		
c 14	42.4		13.2	514	6	CA248787	CG178817 PUF505TB		
c 15	42.4		13.2	809	7	CG178817	CG178819 PUF505TB		
c 16	42.4		13.2	906	9	CG178817	CG178819 PUF505TB		
c 17	42.4		13.2	912	9	CG178819	CG08181 PUDR6TB		
c 18	42.4		13.2	958	9	CG08181	CC667226 OGUE733TV		
c 19	42.4		13.2	960	9	CNS667226	CP482726 POL1_72D		
c 20	42.2		13.1	734	7	CP482726	BI776880 EBP103_SQ		
c 21	42		13.1	323	4	BI776880	BUS983832 HA31C72r		
c 22	42		13.1	429	5	BUS983832	CD895551 G174_1.00C		
c 23	42		13.1	530	6	CD895551	CD902568 G356_1.07G		
c 24	42		13.1	638	6	CD902568			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1

CNS0091P LOCUS CNS0091P, 925 bp DNA, linear GSS 03-JUN-1999 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL053013

VERSION AL053013.1 GI:4934461

KEYWORDS GSS.

SOURCE Drosophila melanogaster

ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydioidea; Drosophilidae; Drosophila.

REFERENCE Genoscope.

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted [02-JUN-1999] Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cnrs.fr)

COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org>. The BDGP Drosophila melanogaster BAC library was prepared by Kazutomo Oisoegawa and Aaron Mammsoer in Pieter Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by the BDGP from the EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers

1 . 925

/organism="Drosophila melanogaster"

/no_type="genomic DNA"

/db_xref="taxon:7227"

/clone=BACR19D16"

/clone lib="RPCI-98"

/note="End : TET3"

ORIGIN

Query Match Score 49.8 ; DB 9 ; Pred. No. 0.024 ; Length 925 ; Best Local Similarity 14.7 % ; Best

FEATURES	source	Location/Qualifiers
	1. 792	/organism="Sorghum bicolor"
	/mol_type="mRNA"	/cultivar="recital"
	/cultivar="Brix623"	/db_xref="taxon:4558"
	/db_xref="taxon:4558"	/clone="GR45100N24"
	/clone="P011_43_H12_A002"	/tissue_type="grain" (45 degrees per day after
	/lab_host="DH10B-T1 phage-resistant E. coli"	pollination)
	/clone lib="Pollen"	/clone lib="GR45"
	/note="Organ: Pollen; Vector: pME18S-FL3; Site 1: XhoI; Site 2: XbaI; The library was prepared from polyA+ RNA from pollen at the late vacuolated stage of development. Pollen was harvested from greenhouse-grown panicles of sorghum line Brix23. Panicles were removed from the flag leaf prior to emergence, when no detectable amylase is present in pollen of male-fertile lines. This stage represents pollen collected from panicles about 8-14 days prior to anthesis. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5'-prime DraIII site is CACTGTTG, 3'-prime DraIII site is GACCCTTG). XbaI excises the cDNA insert."	
ORIGIN		
	Query Match 14.6%; Score 46.8; DB 7; Length 792;	
	Best Local Similarity 50.4%; Pred. No. 0.14; Matches 114; Conservative 0; Mismatches 112; Indels 0; Gaps 0;	
	Db 753 CGCGCAGGGCTAACCCCCCCTGGATGGCGCACATGGTGGCCGC 95	
	Qy 36 CGACGTTCGGTGGCGGAGACGGCAGATGGCGTGGCGATGGCG 155	
	Db 693 AGAGGCCAGGTGGTGGAGAGCTGGCGAGAGCTGGCTGGCT 634	
	Qy 96 CGGAGCTAACCCGGATGGTGGCGACATCACAGAAATTGAGGACAGCGCAACT 215	
	Db 633 CGAGGTGAGGTGAGCTGGTAGGAGCTGGCGGAGCTGGCGACT 574	
	Qy 216 GCGGCTTGTGATGGCATCTGGAGCTGGCGCTTGAG 261	
	Db 573 GTAGATGAGCTGGCCATGGTGGCGAGCTGGCTGAG 528	
ORIGIN		
	Query Match 14.1%; Score 45.2; DB 6; Length 626;	
	Best Local Similarity 49.6%; Pred. No. 0.36; Matches 116; Conservative 0; Mismatches 118; Indels 0; Gaps 0;	
	Qy 44 GGCTCAACGCCCGCGTCGAATGGCTGGCGAACATGGTGGCGCCGAGCTTC 103	
	Db 609 GGCACGGGAACCGGTGGCGGAAACCGTAACGGCTGGCTGCTGCTTC 550	
	Qy 104 CGTCCCCGAGCAGCCGGCCCAACGGGAGCGAACCTGAGGGTATCGCCGAGCTG 163	
	Db 549 CCTCCCGGGCTTGGCTCTGGCCAGCTCTCGCCAGCTCGAACGGCTGTAGTCCTCCGGCG 490	
ORIGIN		
	Query Match 14.1%; Score 45.2; DB 6; Length 626;	
	Best Local Similarity 49.6%; Pred. No. 0.36; Matches 116; Conservative 0; Mismatches 118; Indels 0; Gaps 0;	
	Qy 44 GGCTCAACGCCCGCGTCGAATGGCTGGCGAACATGGTGGCGCCGAGCTTC 103	
	Db 609 GGCACGGGAACCGGTGGCGGAAACCGTAACGGCTGGCTGCTGCTTC 550	
	Qy 104 CGTCCCCGAGCAGCCGGCCCAACGGGAGCGAACCTGAGGGTATCGCCGAGCTG 163	
	Db 549 CCTCCCGGGCTTGGCTCTGGCCAGCTCTCGCCAGCTCGAACGGCTGTAGTCCTCCGGCG 490	
RESULT 5		
	CNS0091P/C	CNS0091P
	LOCUS	Drosophila melanogaster genome survey sequence TET3 end of BAC #
	DEFINITION	BACR19D16 of BACR198 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
	ACCESSION	AL053013
	VERSION	AL053013.1
	KEYWORDS	GI:4934461
	SOURCE	Drosophila melanogaster (fruit fly)
	ORGANISM	Drosophila melanogaster
	COMMENT	Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidea; Drosophilidae; Drosophila.
	REFERENCE	1 (bases 1 to 925)
	AUTHORS	Genoscope.
	TITLE	Direct Submission
	JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
	DEFINITION	- Web : www.genoscope.cns.fr.
	KEYWORDS	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
	ORGANISM	The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org. The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoer in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2, cn bw sp, the same strain used for the library P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm
	COMMENT	Location/Qualifiers
RESULT 4		
	CD927090/C	CD927090
	LOCUS	626 bp mRNA linear EST 15-JUL-2003
	DEFINITION	EST. mRNA sequence.
	ACCESSION	CD927090
	VERSION	1 GI:32774854
	KEYWORDS	EST.
	ORGANISM	Triticum aestivum (bread wheat)
	REFERENCE	Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Triticum.
	AUTHORS	1 (bases 1 to 626)
	TITLE	Genoplante.
	JOURNAL	Genoplante, a major partnership french program in plant genomics unpublished (2003)
	COMMENT	Contact: Genoplante 93 rue Henri Rochefort 91025 EVRY CEDEX France Tel: 33 1 69 47 54 00 Fax: 33 1 69 47 54 10
FEATURES		This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com) and http://genoplante-info.biogen.fr .
	source	Location/Qualifiers
	1. .626	1. organism="Drosophila melanogaster"
	/mol_type="genomic DNA"	/mo_type="genomic DNA"
	/db_xref="taxon:7227"	/db_xref="taxon:7227"
	/clone="BACR19D16"	/clone="BACR19D16"
	/clone_lib="RPCI-98"	/clone_lib="RPCI-98"
	/note="end : TET3"	/note="end : TET3"

Db	482	ACGTGATCAAGCGGGCAAAGAGCTGCCATGGGATCGGATCGAAC	531	Eukaryota; Alveolata; Apicomplexa; Coccidia; Bimerida; Sarcobiontida; Toxoplasma.
RESULT	8			
P305L	P305L	623 bp DNA end-linear GSS 16-MAR-2000		REFERENCE Tang, K., Cole, R., Rogarty, S., Sibley, L.D., Ajioka, J.A., White, M., Clifton, S., Pape, D.P., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theisinger, B., Bowers, Y., Gibbons, M., Ritter, F., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.
DEFINITION Leishmania major Friedlin PAC P305 left end sequence, similar to ECPBN D90227 Escherichia coli phn operon genes. . . , N=835, Prob>7.2e-59; SW:PHND_ECOLI_P16562 PHOSPHONATES-BINDING. . . , N=480, Prob<1.e-61, genomic survey sequence.				AUTHORS Toxoplasma EST Project Unpublished (2001) Contact: Clifton, S.
ACCESSION AL160634	AL160634..1	GI:7259018		JOURNAL Toxoplasma EST Project COMMENT Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: toxowebson.wustl.edu
KEYWORDS				Contact David Sibley (toxocim.wustl.edu) for further information relating to organism, libraries, or clone availability.
SOURCE				Seq primer: -40RP from Gibco High quality sequence stop: 439.
ORGANISM Leishmania major				Location/Qualifiers
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;				1. organism="Toxoplasma gondii" /mol_type="mRNA" /strain="RH (Type I)" /db_xref="taxon:5611"
Leishmania.				/clone="TgBENzyd65f02.y2" /dev_stage="Tachyzoite" /lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
1 (bases 1 to 623)				/clone_lib="TgRH Tachyzoite Norm 5 cDNA Library" /note="Vector: pBluescript SK+ Site 1: EcoRI; Site 2: XbaI; Toxoplasma RH strain tachyzoites were grown in human foreskin fibroblast cultures in vitro. The library was originally constructed by K.L.Wan, Cambridge University. cDNAs were synthesized from polyA RNAs by oligo d(T) priming and directionally cloned into the EcoRI to XbaI sites of the Lambda ZapII vector using the ZAP-cDNA synthesis kit (Stratagene). The primary cDNA library was mass excised as phagemid using EXASpell helper phage (Stratagene). Phagemid DNA was extracted by phenol-chloroform method, and hybridized against a pool of highly abundant genes which were derived from short-cycle PCR of the primary cDNA library. The normalized library was electroporated into DH10B (GeneHog, Invitrogen, Inc.).
REFERENCE				WARNING: the library contains a small percentage of cDNAs derived from the human host cells."
AUTHORS Ivens, A.C., Lewis, S.M., Bagherzadeh, A., Zhang, L., Chan, H.M. and Smith, D.F.				
TITLE A physical map of the Leishmania major Friedlin genome				
MEDLINE 98146435				
PUBMED 9477341				
REFERENCE 2 (bases 1 to 173)				
AUTHORS Taylor, R.G., Huckle, E.B.J., Ivens, A.C., Rajandream, M.A. and Barrell, B.G.				
TITLE Direct Submission				
JOURNAL Submitted (14-MAR-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK, E-mail: barrell@sanger.ac.uk and alicat@sanger.ac.uk				
COMMENT See http://www.ebi.ac.uk/parasites/leish.html Details of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/L_major/ The primer sequence can be obtained from alicat@sanger.ac.uk.				
FEATURES				
SOURCE				
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AUTHORS Taylor, R.G., Huckle, E.B.J., Ivens, A.C., Rajandream, M.A. and Barrell, B.G.				
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TITLE Direct Submission				
JOURNAL Submitted (14-MAR-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK, E-mail: barrell@sanger.ac.uk and alicat@sanger.ac.uk				
COMMENT See http://www.ebi.ac.uk/parasites/leish.html Details of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/L_major/ The primer sequence can be obtained from alicat@sanger.ac.uk.				
FEATURES				
SOURCE				
REPRIMER 1..623				
AUTHORS Taylor, R.G., Huckle, E.B.J., Ivens, A.C., Rajandream, M.A. and Barrell, B.G.				
TITLE Direct Submission				
JOURNAL Submitted (14-MAR-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK, E-mail: barrell@sanger.ac.uk and alicat@sanger.ac.uk				
COMMENT See http://www.ebi.ac.uk/parasites/leish.html Details of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/L_major/ The primer sequence can be obtained from alicat@sanger.ac.uk.				
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SOURCE				
REPRIMER 1..623				
AUTHORS Taylor, R.G., Huckle, E.B.J., Ivens, A.C., Rajandream, M.A. and Barrell, B.G.				
TITLE Direct Submission				
JOURNAL Submitted (14-MAR-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK, E-mail: barrell@sanger.ac.uk and alicat@sanger.ac.uk				
COMMENT See http://www.ebi.ac.uk/parasites/leish.html Details of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/L_major/ The primer sequence can be obtained from alicat@sanger.ac.uk.				
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SOURCE				
REPRIMER 1..623				
AUTHORS Taylor, R.G., Huckle, E.B.J., Ivens, A.C., Rajandream, M.A. and Barrell, B.G.				
TITLE Direct Submission				
JOURNAL Submitted (14-MAR-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK, E-mail: barrell@sanger.ac.uk and alicat@sanger.ac.uk				
COMMENT See http://www.ebi.ac.uk/parasites/leish.html Details of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/L_major/ The primer sequence can be obtained from alicat@sanger.ac.uk.				
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SOURCE				
REPRIMER 1..623				
AUTHORS Taylor, R.G., Huckle, E.B.J., Ivens, A.C., Rajandream, M.A. and Barrell, B.G.				
TITLE Direct Submission				
JOURNAL Submitted (14-MAR-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK, E-mail: barrell@sanger.ac.uk and alicat@sanger.ac.uk				
COMMENT See http://www.ebi.ac.uk/parasites/leish.html Details of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/L_major/ The primer sequence can be obtained from alicat@sanger.ac.uk.				
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REPRIMER 1..623				
AUTHORS Taylor, R.G., Huckle, E.B.J., Ivens, A.C., Rajandream, M.A. and Barrell, B.G.				
TITLE Direct Submission				
JOURNAL Submitted (14-MAR-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK, E-mail: barrell@sanger.ac.uk and alicat@sanger.ac.uk				
COMMENT See http://www.ebi.ac.uk/parasites/leish.html Details of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/L_major/ The primer sequence can be obtained from alicat@sanger.ac.uk.				
FEATURES				
SOURCE				
REPRIMER 1..623				
AUTHORS Taylor, R.G., Huckle, E.B.J., Ivens, A.C., Rajandream, M.A. and Barrell, B.G.				
TITLE Direct Submission				
JOURNAL Submitted (14-MAR-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK, E				

/db_xref="taxon:287"
 /clone="msh2_2505"
 /clone.lib="msh"
 /note="Environmental isolate. Whole genomic shotgun library."

ORIGIN

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 Best Local Similarity 37.3%; Pred. No. 1.6;
 Matches 51; Conservative 36; Mismatches 50; Indels 0; Gaps 0;

Query Match 13.3%; Score 42.8; DB 8; Length 1348;
 Best Local Similarity 50.5%; Pred. No. 1.4;
 Matches 104; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

Qy 48 CAACGCCCGGTGCGGAAATCCGTTGGGCAAACATGGTGGCCAGACGTTCCGTC
 Db 410 CCACGTCTGTGACGGAACATGATGGCTGGCGGACAGATGTTGG 351

Qy 108 CGCCGAGCAGGCGGACCTTCAGCGCCAGGGTACCG 167
 Db 350 TGGACATCATAGCGGCGCTTCAGCTGGCGGACTGGACGG 291

RESULT 14 CA248787 514 bp mRNA linear EST 25-SEP-2003
 LOCUS SC5BFL1.04G10.9 FL1 Saccharum officinarum cdNA clone SC5BFL1.04G10

DEFINITION SC5BFL1.04G10.9 mRNA sequence
 CA248787 5' mRNA sequence

ACCESSION CA248787.1 GI:35330788
 VERSION EST.

KEYWORDS EST.

ORGANISM Saccharum officinarum
 Saccharum officinarum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Sporophyta; Magnoliidae; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
 complex.

REFERENCE 1 (bases 1 to 514)
 Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

AUTHORS The libraries that made SUCEST

TITLE Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

JOURNAL Contact: Arruda P

COMMENT Centro de Biologia Molecular e Engenharia Genética
 Universidade Estadual de Campinas
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Phone: 55 19 3788 1137
 Fax: 55 19 3788 1089
 Email: Parruda@unicamp.br

Clone distribution: Clone distribution information can be found
 through the Brazilian Clone Collection Center (BCCC) at
<http://www.bcccenter.fcav.unesp.br>

Plate: 104 row: G column: 10
 Seq primer: T7 Promoter Primer.

Location/Qualifiers 1..514

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 /organism="Saccharum officinarum"
 /mol type="mRNA"

/db_xref="taxon:4547"
 /clone="SC5BFL1.04G10"
 /lab host="DE10B"
 /clone lib="FL1"
 /note="Organ: Inflorescence at beginning of development
 (1cm-long); Vector: pSPRI; Site 1: SalI; Site 2: NotI;
 An unidirectional cDNA library generated from
 [inflorescence at beginning of development (1cm-long)].
 cDNA was prepared from polyA+ mRNA using SuperScript
 Plasmid System Kit (Invitrogen). The double-strand cDNAs
 were fractionated in a Sepharose CL-2B 40cm-columns and
 fragments sizing between 0.8 and 1.5 Kb were
 directionally cloned into the vector. Details of each
 source of RNA and library construction can be obtained at
<http://sucest.lad.ic.unicamp.br/public/>

FEATURES

Source
 /organism="Drosophila melanogaster"
 /mol type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACR14B09"
 /clone.lib="BACR14B09"
 /note="End : T7"

ORIGIN

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 Best Local Similarity 49.3%; Pred. No. 1.9;
 Matches 109; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

Qy 92 CGGGCGACGTTCCGTCGGCGSAGCGCGGCCAACGGCAGGCCGACCTCGAGGCTA 151

search completed: February 10, 2005, 06:43:13
 job time : 2108 secs

RESULT 15

CC626073/c

LOCUS CC626073 809 bp DNA linear GSS 19-JUN-2003

DEFINITION genomic survey sequence.

ACCESSION CC626073

VERSION 1 GI:31995181

KEYWORDS GSS, Zea mays

ORGANISM Zea mays; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE Whitelaw,C.A., Quackenbush,J.J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Nurnberg,P., Budiman,M.A., Bedell,J.A., Citek,R.W., Robbins,D., Nunberg,A., Rohlfing,T., Lakey,N., Consortium for Maize Genomics Unpublished (2002)

AUTHORS Other GSS: OGUFH43TH

COMMENT Contact: Cathy Whitelaw

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA

FEATURES

source	location/qualifiers
1. 809	/organism="Zea mays" /mol type="genomic DNA" /strain="BT3" /db_xref="taxon:4577"
	/clone lib="ZMMBa0439H4" /clone lib="2M_0_7-1.5_KB" /note="Vector: PBCK; Site:1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"

ORIGIN

Query Match	Score	DB	Length
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Matches	53.7%	Pred. No. 1, 8;	
88; Conservative	0;	Mismatches	0; Gaps 0;

Qy 152 TCCGCCAGCTACGGAGATCAACCTTCCTGCGGAGAAATCGAGCACAGCCG 211

Qy 353 TGGGCCTGCCAAGGTGGCGCTGGGAGCCCTGGGAGCCCTGGGAGCCACG 412

Db 212 AACTGGGGCTGTTGTCATGATCTTGACATGAGGGGGATGA 271

Db 413 TCCTGGCCCTCCGGGACCTCTGGGATCTGGGGCATCTGGGGCACGGT 472

Qy 272 AGCTCGGCTGGATCCTATCGGTACTTCCCAGGAATCCGAC 312

Db 473 CGCTGGCGGNGACTCCGCCGCGTCCGACGGCGGAC 513

XX	Sequence 324 BP; 69 A; 112 C; 100 G; 43 T; 0 U; 0 Other;	WP	AAI99682_36	3710000
SQ	Query Match 100.0%; Score 321; DB 4; Length 324; Best Local Similarity 100.0%; Pred. No. 5.9e-70; Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	WP	AAI99682_17	3700001
Qy	1 TTGACCCACAAAGCGACTAACGGCAAGGCCATGGCTAACGCCGCGGT 60 Db 1 TTGACCCAAAGCGACTAACGGCAAGGCCATGGCTAACGCCGCGGT 60	WP	AAI99682_38	3810000
Qy	61 CGGAATCGGTTGGCGGAAACATGGTGGCGGAGTCGGTCCGGCAGGGC 120 Db 61 CGGAATCGGTTGGCGGAAACATGGTGGCGGAGTCGGTCCGGCAGGGC 120	WP	AAI99682_39	3900001
Qy	121 CGGCCCAAGGCCACCTCGAGGTATCGCGGAGCGTACGGCGAGTGGCG 180 Db 121 CGGCCCAAGGCCACCTCGAGGTATCGCGGAGCGTACGGCGAGTGGCG 180	WP	AAI99682_40	4000001
Qy	181 ACATACACAAATTGACCGACGAACAGCCGAAACTGGCGCTGTTGTCGATCTCAC 240 Db 181 ACATACACAAATTGACCGACGAACAGCCGAAACTGGCGCTGTTGTCGATCTCAC 240	WP	AAI99682_41	4100001
Qy	241 GATGAGCACGCCGCCTTGAGGGGGATGAAGCTCGCTGGCATCGTACTTCGC 300 Db 241 GATGAGCACGCCGCCTTGAGGGGGATGAAGCTCGCTGGCATCGTACTTCGC 300	WP	AAI99682_42	4200001
Qy	301 GACGAACCCGACAGCAAAAG 321 Db 301 GACGAACCCGACAGCAAAAG 321	WP	AAI99682_43	4310000
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Qy	1 TTGACCCACAAAGCGACTAACGGCAAGGCCATGGCTAACGCCGCGGT 60 Db 76906 TTGACCCACAAAGCGACTAACGGCAAGGCCATGGCTAACGCCGCGGT 76847	WP	AAI99682_45	4400001
Qy	61 CGGAATCGGTTGGCGGAAACATGGTGGCGGAGTCGGGAGATGGTGGCG 180 Db 76846 CGGAATCGGTTGGCGGAAACATGGTGGCGGAGTCGGGAGATGGTGGCG 180	WP	AAI99682_46	4510000
Qy	121 CGGCCCAAGGCCACCTCGAGGTATCGCGGAGCGTACGGCGAGTGGCG 180 Db 76786 CGGCCCAAGGCCACCTCGAGGTATCGCGGAGCGTACGGCGAGTGGTGGCG 76727	WP	AAI99682_47	4610000
Qy	181 ACATACACAAATTGACCGACGAACAGCCGAAACTGGCGCTGTTGTCGATCTCAC 240 Db 76726 ACATACACGAATTGACCGACGAACAGCCGAAACTGGCGCTGTTGTCGATCTCAC 240	WP	AAI99682_48	4710000
Qy	241 GATGAGCACGCCGCCTTGAGGGGGATGAAGCTCGCTGGCATCGTACTTCGC 300 Db 76666 GATGAGCACGCCGCCTTGAGGGGGATGAAGCTCGCTGGCATCGTACTTCGC 300	WP	AAI99682_49	4810000
Qy	301 GACGAACCCGACAGCAAAAG 321 Db 76606 GACGAACCCGACAGCAAAAG 321	WP	AAI99682_50	4910000
RESULT 3 AAI99682_29/C Continuation (30 of 45) of AAI99682 from base 2900001 (Mycobacterium tuberculosis strain WP Sequence split into 45 fragments LOCUS AAI99682 Accession AAI99682				
WP	Fragment Name Begin End	WP	AAI99682_00	1
WP	AAI99682_01	100001	110000	
WP	AAI99682_02	200001	310000	
WP	AAI99682_03	300001	410000	
WP	AAI99682_04	400001	510000	
WP	AAI99682_05	500001	610000	
WP	AAI99682_06	600001	710000	
WP	AAI99682_07	700001	810000	
WP	AAI99682_08	800001	910000	
WP	AAI99682_09	900001	1010000	
WP	AAI99682_10	1000001	1110000	
WP	AAI99682_11	1100001	1210000	
WP	AAI99682_12	1200001	1310000	
WP	AAI99682_13	1300001	1410000	
WP	AAI99682_14	1400001	1510000	
WP	AAI99682_15	1500001	1610000	
WP	AAI99682_16	1600001	1710000	
WP	AAI99682_17	1700001	1810000	
WP	AAI99682_18	1800001	1910000	
WP	AAI99682_19	1900001	2010000	
WP	AAI99682_20	2000001	2110000	
WP	AAI99682_21	2100001	2210000	
WP	AAI99682_22	2200001	2310000	
WP	AAI99682_23	2300001	2410000	
WP	AAI99682_24	2400001	2510000	
WP	AAI99682_25	2500001	2610000	
WP	AAI99682_26	2600001	2710000	
WP	AAI99682_27	2700001	2810000	
WP	AAI99682_28	2800001	2910000	
WP	AAI99682_29	2900001	3010000	
WP	AAI99682_30	3000001	3110000	
WP	AAI99682_31	3100001	3210000	
WP	AAI99682_32	3200001	3310000	
WP	AAI99682_33	3300001	3410000	
WP	AAI99682_34	3400001	3510000	
WP	AAI99682_35	3500001	3610000	
RESULT 3 AAI99683_29/C Continuation (30 of 44) of AAI99683 from base 2900001 (Mycobacterium tuberculosis strain WP Sequence split into 44 fragments LOCUS AAI99683 Accession AAI99683				
WP	Fragment Name Begin End	WP	AAI99683_00	1
WP	AAI99683_01	100001	210000	
WP	AAI99683_02	110001	310000	
WP	AAI99683_03	300001	410000	
WP	AAI99683_04	400001	510000	
WP	AAI99683_05	500001	610000	
WP	AAI99683_06	600001	710000	
WP	AAI99683_07	700001	810000	
WP	AAI99683_08	800001	910000	
WP	AAI99683_09	900001	1010000	
WP	AAI99683_10	1000001	1110000	
WP	AAI99683_11	1100001	1210000	
WP	AAI99683_12	1200001	1310000	
WP	AAI99683_13	1300001	1410000	
WP	AAI99683_14	1400001	1510000	
WP	AAI99683_15	1500001	1610000	
WP	AAI99683_16	1600001	1710000	
WP	AAI99683_17	1700001	1810000	
WP	AAI99683_18	1800001	1910000	
WP	AAI99683_19	1900001	2010000	
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WP	AAI99683_33	3300001	3410000	
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WP	AAI99683_35	3500001	3610000	

XX (ELIT-) ELITRA PHARM INC.
 XX PA
 XX PI Haselbeck R, Olsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 XX PI Yamamoto RT, Xu HH;
 XX DR WPI; 2001-61149570.
 P-PSDB; AU03683.
 XX PR New polynucleotides for the identification and development of
 PR antibiotics, comprise sequences of antisense nucleic acids.
 XX PR
 XX Claim 27; SEQ ID NO 4124; 511pp; English.
 XX PS
 XX The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia
 CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
 CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence encodes an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Query Match 100 %; Score 321; DB 4; Length 110000;
 Best Local Similarity 100 %; Pred. No. 9.9e-70; Indels 0; Gaps 0;
 Matches 321; Conservative 0; Mismatches 0;
 CC 1 TGACCAACAGCGCCTAAACGCCAGCCACCATGCCGAGGGCTCAAAGCCCGCGT 60
 Db 71654 TGACCAACAGGCACACTAACGCCACCCAGCACCTGGCTCAAACCCCGCT 71595
 Qy 61 CGGAATGCGTTGGCGCAACATGGTTGGCGGCCACGTTTCGCGCAAGCAGCGC 120
 Db 71594 CGGAATGCGTTGGGGCAACATGGTTGGGGCCACGTTTCGCGCCAGCAGCGC 71535
 Qy 121 CGGCCCCAACCCAGCCGACA CCTCGAGCTAACCGCGGAGGTACCGCGAATGGTGGCG 180
 Db 71534 CGGCCAACCCAGCCGACA CCTCGAGCTAACCGCGGAGGTACCGCGAATGGTGGCG 71475
 Qy 181 ACATCACAGAAATCGACGCCAACAGCCGACA CGCCGAACTGGCGCTTGCGATCGAC 240
 Db 71474 ACATCACAGAAATCGACGCCAACAGCCGACA CGCCGAACTGGCGCTTGCGATCGAC 71415
 Qy 241 GATGAGCAGCGCGGCTTGAGCGGGATGAGCTCGCTGGCATCGTAACTTCGCC 300
 Db 71414 GATGAGCAGCGCGGCTTGAGCGGGATGAGCTCGCTGGCATCGTAACTTCGCC 71355
 Qy 301 GACGAACCGCACAGCAAAGC 321
 Db 71354 GACGAACCCGACAGAACAG 71334
 RESULT 4
 AAS51542/c
 ID AAS51542 standard; DNA; 4200 BP.
 KW Antisense; ds: prokaryotic cellular proliferation gene; antibiotic;
 KW antibacterial; drug design.
 XX Pseudomonas aeruginosa.
 XX OS WO200170955-A2.
 XX PN 27-SEP-2001.
 XX DT 13-FEB-2002 (first entry)
 XX DB Pseudomonas aeruginosa DNA for cellular proliferation protein #127.
 XX DE RESULT 5
 ID ACA19522/c
 ID ACA19522 standard; DNA; 4200 BP.
 XX AC ACA19522;
 XX DT 19-JUN-2003 (first entry)
 XX DE Prokaryotic essential gene #1179.
 XX KW Antisense; ds: prokaryotic essential gene; cell proliferation;
 KW drug design; gene.
 XX OS Pseudomonas aeruginosa.
 XX PN WO20027183-A2.
 PR 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-020772P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-025365P.
 PR 16-FEB-2001; 2000US-025931P.
 PR 22-DEC-2001; 2000US-0259308P.

PD	03-OCT-2002.	Qy	228 GATGCATCTCGACGATGAGCAGGCC 253
XX	21-MAR-2002; 2002NO-US009107.	Db	1339 TCGCTTCCTCGATGAGGCC 1314
XX	21-MAR-2001; 2001US-00815242.		RESULT 6
PR	06-SEP-2001; 2001US-00948993.		ABD06144/C
PR	06-OCT-2001; 2001US-034293P.		ABD06144 standard; DNA; 4212 BP.
PR	08-FEB-2002; 2002US-00072851.		
PR	06-MAR-2002; 2002US-032695P.		
XX	(ELIT-) ELITRA PHARM INC.		
PA			
XX	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;		
PI	Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA,		
XX	Xu HH;		
DR	WPI; 2003-029926/02.		Pseudomonas aeruginosa infection; gene; ds; Pseudomonas aeruginosa infection;
XX	P-PSDB; AB015652.		
PT	New antisense nucleic acids, useful for identifying proteins or screening		
PT	for homologous nucleic acids required for cellular proliferation to		
PT	isolate candidate molecules for rational drug discovery programs.		Pseudomonas aeruginosa.
XX	Claim 14, SEQ ID NO 7392; 1766pp; English.		
XX	The invention relates to an isolated nucleic acid comprising any one of		
CC	the 6213 antisense sequences given in the specification where expression		
CC	of the nucleic acid inhibits proliferation of a cell. Also included are:		
CC	(1) a vector comprising a promoter operably linked to the nucleic acid		
CC	encoding a polypeptide whose expression is inhibited by the antisense		
CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated		
CC	polypeptide or its fragment whose expression is inhibited by the		
CC	antisense nucleic acid; (4) an antibody capable of specifically binding		
CC	the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular		
CC	proliferation or the activity of a gene in an operon required for		
CC	proliferation; (7) identifying a compound that influences the activity of		
CC	the gene product or that has an activity against a biological pathway		
CC	required for proliferation, or that inhibits cellular proliferation; (8)		
CC	identifying a gene required for cellular proliferation or the biological		
CC	pathway in which a proliferation-required product lies		
CC	or a gene on which the test compound that inhibits proliferation of an		
CC	compound's activity; (9) manufacturing an antibiotic; (10) profiling a		
CC	product which each of the strains is present in a culture or collection of		
CC	strains; or (11) identifying the target of a compound that inhibits the		
CC	proliferation of an organism. The antisense nucleic acids are useful for		
CC	identifying proteins or screening for homologous nucleic acids required		
CC	for cellular proliferation to isolate candidate molecules for rational		
CC	drug discovery programs, or for screening homologous nucleic acids		
CC	required for proliferation in cells other than S. aureus, S. typhimurium,		
CC	K. pneumoniae or P. aeruginosa. The present sequence is one of the target		
CC	prokaryotic essential genes. Note: The sequence data for this patent did		
CC	not form part of the printed specification, but was obtained in		
CC	electronic format directly from WIPO at		
XX	http://wipo.int/pub/published_pct_sequences		
SQ	Sequence 4200 BP; 846 A; 1329 C; 1304 G; 721 T; 0 U; 0 Other;		
Query Match	13.3%;	Score 42.8;	DB 8;
Best Local Similarity	50.5%;	Length 4200;	
Matches	104;	Pred. No. 0.42;	
	Conservative	0;	Mismatches 102;
		Indels 0;	Gaps 0;
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Db	1519 CCAGCTCTGGCGACGGAAACATGGTTGGGGCAACAGGATGTTGG 1460		Best Local Similarity 50.5%; Pred. No. 0.42;
Qy	108 CGCGGAGGAGCGCCGAGCGACGCGAACGAGGAGAATGAGCAGAGAACGCGAACCTGGCTGTGTC 167		Matches 104; Conservative 0; Mismatches 102;
Db	1459 TGGACATCTCAAGCGGCGCTTGCGCTTCACTGGCGCTGGGGTCAAGGAACGTTGGACCG 1400		Sequence 4212 BP; 850 A; 1338 C; 1311 G; 713 T; 0 U; 0 Other;
Qy	168 CGAGATGGTGGGACATCACAGGAATTGAGCAGACAAGCGGAACCTGGCTGTGTC 227		Query Match 48 CAACGCCCGCGTGGATCGCGTGGGGCGCAACTGGTGGCGCCGAGCGTC 107
Db	1399 CCATCTGTCACCGTCAAGTGGCTTCAAGCTGGGCGCTCAGGAACTGGCTACGGGACGG 1340		Best Local Similarity 50.5%; Pred. No. 0.42;
			Matches 104; Conservative 0; Mismatches 102;
			Sequence 4212 BP; 850 A; 1338 C; 1311 G; 713 T; 0 U; 0 Other;
Qy	108 CGCGGAGGAGCGCCGAGCGACGCGAACGAGGAGAATGAGCAGAGAACGCGAACCTGGCTGTGTC 167		Query Match 48 CAACGCCCGCGTGGATCGCGTGGGGCGCAACTGGTGGCGCCGAGCGTC 107
Db	1531 CCACGTCCTGCGACGAGATGATGCTGGCTGGCGCTGGGGTCAAGGAACGTTGGACCG 1472		Best Local Similarity 50.5%; Pred. No. 0.42;
Qy	108 CGCGGAGGAGCGCCGAGCGACGCGAACGAGGAGAATGAGCAGAGAACGCGAACCTGGCTGTGTC 167		Matches 104; Conservative 0; Mismatches 102;
Db	1471 TGGACATCTCAAGCGGCGCTTGCGCTTCAAGCTGGGCGCTCAGGAACTGGCTACGGGACGG 1412		Sequence 4212 BP; 850 A; 1338 C; 1311 G; 713 T; 0 U; 0 Other;

Qy	168	CGAGATGGTGCAGCATCACAGAAATCTGAGACAGCCGAACTGGGCTTTGTC	227	Db	1411	CCATCTGGTACCGTGTGAAGTGTGGCTTAGCGGGAGACCCGGGGAGCTGGA	1352
Qy	228	GATGCATCTGACGATGAGCAGGCC	253	Db	1351	TGCGCTTGCGCTCGATGAGGACCGC	1326
RESULT 7 ABD06093	ID	ABD06093 standard; DNA; 4242 BP.					
XX	AC	ABD06093;					
XX	DT	29-JUL-2004 (First entry)					
XX	DE	Pseudomonas aeruginosa polynucleotide #4697.					
XX	KW	Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;					
XX	KW	antibacterial.					
XX	OS	Pseudomonas aeruginosa.					
XX	PN	US6551795-B1.					
XX	PD	22-APR-2003.					
XX	PP	18-FEB-1999; 99US-00252991.					
XX	PR	18-FEB-1998; 98US-0074788P.					
XX	PR	27-JUL-1998; 98US-0094190P.					
XX	(GENO-) GENOME THERAPEUTICS CORP.						
XX	PA	Rubenfield MJ, Nolling J, Deloughery C, Bush D;					
XX	PI	WPI; 2003-615309/58.					
XX	DR	P-PSDB; ABO72522.					
XX	PT	Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics. Prophylaxis and treatment of pathological conditions resulting from bacterial infection.					
PT	Disclosure: SEQ ID NO 4697; 45SPP; English.						
XX	The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABD01397-ABD17967 represent P. aeruginosa polynucleotides of the invention. Note: The sequence data for this patient did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html						
XX	Sequence 4242 BP; 717 A; 1322 C; 1348 G; 855 T; 0 U; 0 Other; Best Local Similarity 50.5%; Score 42.8; DB 11; Length 4242; Matches 104; Conservative 0; Mismatches 102; Indels 0; Gaps 0;						
SQ	Query Match 13.3%; Score 42.8; Pred. No. 0.42;						
Qy	48 CAACGCCGCCGCTGCGAATCGGTRGGGCCAACATGGTGGCGGCCAGCTTCGGTC 107						
Db	2685 CCACGCCCTGGGACGAAACGATGATGCGCTGGCCAGCTGGTGG 2744						

CC product is overexpressed or underexpressed; (12) determining the extent CC to which each of the strains is present in a culture or collection of CC strains; or (13) identifying the target of a compound that inhibits the CC proliferation of an organism. The antisense nucleic acids are useful for CC identifying proteins or screening for homologous nucleic acids required CC for cellular proliferation to isolate candidate molecules for rational CC drug discovery programs, or for screening homologous nucleic acids CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*, CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target CC prokaryotic essential genes. Note: The sequence data for this patent did CC not form part of the printed specification, but was obtained in an CC electronic format directly from WIPO at CC ftp://wipo.int/pub/published_pct Sequences

SQ Sequence 10232 BP; 1443 A; 3537 C; 3647 G; 1605 T; 0 U; 0 Other;

Query Match Score 42.8; DB 8; Length 10232;
Best Local Similarity 47.7%; Pred. No. 0 45; Mismatches 0; Indels 0; Gaps 0;
Matches 125; Conservative 0; Mismatches 137; Indels 0; Gaps 0;
Qy 20 AACGCCAGCCAGGCCATCGGCCAGGGCTAACGCCCGGCTGGAAATGCCGTTGGC 79
Db 1271 AACGTGCTGACCCGCGTCACCGTGGACAACTGGCTCCGGCGCTGA 1330
Qy 80 AACATGGTGGGGCCGCGGCGTCCGGCCAGCACGCCGCCCAACGCCAGGCC 139
Db 1331 CGAGCCCCACCGCCGGGTCGATCCCCGGCTTCGGAAACCGTCAGGCCA 1390
Qy 140 ACCTGGAGGCTATGCCAAGCTAGGGAGATGGTGAGCATCAAGAAATCCAG 199
Db 1391 CCCCGACCGGGTGGGGTGAACCTTCGGCCGACCTCTGGCTGACCTAGGCCAGC 1450
Qy 200 AGGACACAGCCGACTGGGGCTGGCTGGCCATCTGACCATCTGCTGGT 259
Db 1451 AGGGTCCACCGGCTGGCCATCTGCTGGCTGGCCATCTGCTGGACTCG 1510
Qy 260 AGGGGGGATGAGCTGGCTG 281
Db 1511 TGGGTGATGTTCCCCTG 1532

RESULT 9

ACR23398 standard, DNA, 996 BP.

AC ACR23398;

XX DT 19-JUN-2003 (first entry)

XX DE Prokaryotic essential gene #5055.

XX Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.

XX PN WO200271183-A2.

XX PD 03-OCT-2002.

XX PR 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948933.

PR 25-OCT-2001; 2001US-0342923P.

PR 09-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362695P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlseni KL,

PI Trawick JD, Carr GJ, Yamamoto R, Forsyth RA,

XX XX Xu HH;

XX AC

DR WPI; 2003-029926/02.
DR P-PSDB; ABU19528.

XX PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

XX PT Claim 14; SEQ ID NO 11268; 1766pp; English.

XX XX The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in an electronic format directly from WIPO at ftp://wipo.int/pub/published_pct Sequences

XX SQ Sequence 996 BP; 138 A; 320 C; 387 G; 151 T; 0 U; 0 Other;

XX SQ Sequence 996 BP; 138 A; 320 C; 387 G; 151 T; 0 U; 0 Other;

Query Match 13.0%; Score 41.6; DB 8; Length 996;
Best Local Similarity 50.3%; Pred. No. 0 73; Mismatches 119; Indels 4; Gaps 1;

Matches 127; Conservative 0; Mismatches 119; Indels 4; Gaps 1;
Qy 29 CAGCCATCGCCAGGCTCAAGGCCGCTCGGATCTGGGTGGGGAAACATGGTT 88
Db 145 CTGCAACGGCGGGCTGGCTGCGTCAATGATGCGGCTGCGCTGGGGAT 204

Qy 89 GGCGCGCGACGCTCCGCGCCGACAGGCCGCCAATGCGGAAATGCGGCGAC 144
Db 205 CGCCAGCGCCGCTGGCTAGCGGGTCACTGGCTGGGCGCCACGGGGCGGC 264

Qy 145 GAGGGCTATCCGCCAGCGTAGGCCGATGGTGGCCACATCACCAAATGCGGCGAC 204
Db 265 GACGGCTGTCCCGGCTGGCTGGGGACAGGTCGGCTGGCGACATGGCGCGCTG 324

Qy 205 ACAGCCAACTGGGGCTGCTGAGATCTGAGATGAGCTGGGGCTGGGGCG 264
Db 325 CGGGCGCATCTGGAAACGGTGAAGCGTGGCTGGACATGTGGGGAAACGGCTGACCGCG 384

Qy 265 GGGATGAGGC 274

Db 385 TTGTCGCAGC 394

RESULT 10
ABL8190
ID ABL81990 standard; cDNA; 400 BP.
XX AC ABL81990;

XX XX 17-MAY-2002 (First entry)
 DT XX Human ovarian cancer related cDNA clone SEQ ID NO:4968.
 DE XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
 KW XX Antisense; ds; prokaryotic essential gene; cell proliferation;
 KW drug design; gene.
 OS XX Mycobacterium bovis.
 Homo sapiens.
 PN XX WO200192381-A2.
 XX OS
 PD XX 06-DBC-2001.
 XX PN
 PP XX 29-MAY-2001; 2001WO-US017756.
 XX PR XX 26-MAY-2000; 2000US-0207484P.
 PA XX (CORSI-) CORIXA CORP.
 PI XX Algate PA, Harlocker SL, Jones R;
 XX DR WPI; 2002-122075/16.
 XX PT Composition for therapy and diagnosis of ovarian cancer comprising
 polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
 polypeptide, antibody specific to polypeptide or T cell expressing
 polypeptide.
 PS XX SEQ ID NO 4968; 489pp; English.
 XX The present invention describes a composition (I) comprising: carriers
 CC and immunostimulants; and a polypeptide (II) of a ovarian tumour
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1)
 CC from the 10912 nucleotide sequences as given in AB1:87934.
 CC (II) encoding (S1) having a sequence (S2), a T cell population of (II),
 CC or antigen presenting cells that express (II). (I) has cyclostatic
 CC activity. An Oligonucleotide (IV) that hybridises to (S1) can be used for
 CC detecting ovarian cancer in a patient's biological sample preferably
 CC serum or ovarian tissue. The method comprises contacting a biological
 CC sample from a patient with (IV), detecting the amount of polynucleotide
 CC hybridising to (IV) and comparing the amount to a predetermined cutoff
 CC value and thereby detecting ovarian cancer in the patient, where the
 CC amount of polynucleotide hybridising to (IV) is detected preferably by
 CC polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is
 CC useful for stimulating and/or expanding T cells specific for an ovarian
 CC tumour protein comprising contacting T cells with (III) or (II). (III) is
 CC useful in design and preparation of ribozyme molecules for inhibiting
 CC expression of the tumour polypeptides and proteins in tumour cells; and
 CC to isolate a full length gene from a suitable library e.g., a tumour cDNA
 CC library using well known techniques
 XX Sequence 400 BP; 57 A; 156 C; 135 G; 52 T; 0 U; 0 Other;
 SQ Query Match 12.8%; Score 41; DB 6; Length 400;
 Best Local Similarity 58.7%; Pred. No. 0.95;
 Matches 71; Conservative 0; Nismatches 50; Indels 0; Gaps 0;
 QY 90 GCGGGCGGAACTTCCTCCGGAGGAGGCCAACGGCAACGGGACCTGGAGC 149
 DB 65 GCGGGAGAGGGCGTCCACATGGCAACCTCGGGCAAGGGCCCTCTCGC 124
 QY 150 TATCCGCCGAGCTAGCCGAGATGTGGGACATCACAGGAATTGAGCAGACAGC 209
 DB 125 CTCCCCCGTTGAGGGAGACATCGGGGAACTGGCTGAGGAGGGGGACTCATC 184
 QY 210 C 210
 DB 185 C 185
 XX Sequence 951 BP; 141 A; 308 C; 329 G; 173 T; 0 U; 0 Other;
 SQ Query Match 12.6%; Score 40.4; DB 8; Length 951;
 CC ftp://wipo.int/pub/published_pct_sequences
 CC Sequence 951 BP; 141 A; 308 C; 329 G; 173 T; 0 U; 0 Other;
 CC ID ACA38286 standard; DNA; 951 BP.

RESULT 11
 ACA38286
 ID ACA38286 standard; DNA; 951 BP.

Best Local Similarity 50.4%; Pred. No. 1.4; Matches 129; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

CC an organism
 XX
 SQ Sequence 954 BP; 142 A; 330 C; 173 T; 0 U; 0 Other;

Query Match 12.6%; Score 40.4%; DB 4;
 Best Local Similarity 50.4%; Pred. No. 1.4;
 Matches 129; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

Qy 72 TGCGCGAACATGGTGGCGGCCGACCTTCGCGAGAGCGGCCAAC 131
 Db 276 TCGCTCAACAGACCTGGGACACTGGCACAGGGTCAACGGTGT 335
 Qy 132 GCAGCCGAACTCGAGGATTCGGCAGGGACAT 185
 Db 336 CAATCGGACTCCGGGAGGACCTAGGGGAGGAGCTAGGGGCTAGGGTGT 395
 Qy 186 ACACGAATACTGAGCAGAACAGCGGAACATGGCCGCTGTTGCGATCTGCAGATGA 245
 Db 396 TGCCATTCTGGTACAACCTAGCGTAACGGCTTGTCAGTTC 455
 Qy 246 GCAGCGCCGCGCTTGAGGGCGGATGAAGCTCGGCTGGCGCATCGTACCTCCGAGA 305
 Db 456 GTCGATTCGGTGTGAGCTGAGTGTGGAGGTCGGCTCCGCGGA 515
 Qy 306 ACCCGACAGCAAACNG 321
 Db 516 GCCGGCAGCAAAAGNG 531

RESULT 12
 AAH51985 standard; DNA; 954 BP.
 XX
 AC AAH51985;
 XX 04-SEP-2001 (first entry)
 DE Mycobacterium tuberculosis potential drug target gene SEQ ID 39.
 KW Drug target; growth; organism viability; characterisation; ds.
 OS Mycobacterium tuberculosis.
 PN WO200135317-A1.
 PD 17-MAY-2001.
 XX
 PR 13-NOV-2000; 2000WO-US0311152.
 XX
 PR 12-NOV-1999; 99US-0165086P.
 PR 12-NOV-1999; 99US-0165124P.
 PR 01-FEB-2000; 2000US-0179531P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PI Eisenberg D, Rotstein SH, Marcotte EM;
 DR , 2001-320193/34.
 DR P-PSDB; AAG81134.
 XX
 PT Identifying nucleotide or polypeptide sequence for use as drug target, between nucleotide or polypeptide sequences, and comparing the sequences.
 PT Providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of

XX Disclosure; Page 76-77; 207pp; English.

XX This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polynucleotide sequences AAH51147 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of

CC an organism
 XX
 SQ Sequence 954 BP; 142 A; 330 C; 173 T; 0 U; 0 Other;

Query Match 12.6%; Score 40.4%; DB 4;
 Best Local Similarity 50.4%; Pred. No. 1.4;
 Matches 129; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

Qy 72 TGCGCGAACATGGTGGCGGCCGACCTTCGCGAGAGCGGCCAAC 131
 Db 276 TCGCTCAACAGACCTGGGACACTGGCACAGGGTCAACGGTGT 335
 Qy 132 GCAGCCGAACTCGAGGATTCGGCAGGGACAT 185
 Db 336 CAATCGGACTCCGGGAGGACCTAGGGGAGGAGCTAGGGGCTAGGGTGT 395
 Qy 186 ACACGAATACTGAGCAGAACAGCGGAACATGGCCGCTGTTGCGATCTGCAGATGA 245
 Db 396 TGCCATTCTGGTACAACCTAGCGTAACGGCTTGTCAGTTC 455
 Qy 246 GCAGCGCCGCGCTTGAGGGCGGATGAAGCTCGGCTGGCGCATCGTACCTCCGAGA 305
 Db 456 GTCGATTCGGTGTGAGCTGAGTGTGGAGGTCGGCTCCGCGGA 515
 Qy 306 ACCCGACAGCAAACNG 321
 Db 516 GCCGGCAGCAAAAGNG 531

RESULT 13
 ACA40430
 ID ACA40430 standard; DNA; 954 BP.
 XX
 AC ACA40430;
 XX DT 19-JUN-2003 (first entry)
 DE Prokaryotic essential gene #22087.
 XX
 KW Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.
 XX
 OS Mycobacterium tuberculosis.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 XX
 PR 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-034223P.
 PR 08-FEB-2002; 2002US-0072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELITRA PHARM INC.
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
 PI Wall D, Trawick JD, Carr GA, Yamamoto R, Forsyth RA,
 XX
 DR WPI; 2003-029926/02.
 DR P-PSDB; ABU36560.
 PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 14; SEQ ID NO 28300; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (8) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. Typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

Sequence 954 BP; 142 A; 309 C; 330 G; 173 T; 0 U; 0 Other;

Score 12.6%; Score 40.4%; DB 8; Length 954;

Best Local Similarity 50.4%; Pred. No. 1.4; Indels 6; Gaps 1;

Matches 129; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

Qy 72 TGGGGCAACATGGTGGGGGCCAACGTTCCGTGCGAGAGGGGCCAAACG 131

Db 276 TCGGCTGCAACAGACGGTGGGGAGACTGGCACAGCAGGAGTTAACCGTGGT 335

Qy 132 GCAGGCCGACATTGAGCTTGAGGCTATCGGGCTGCGGGACATC 185

Db 336 CAATCGCACTCCCTGGCCCTGGGGAGATCTAGGCCGGCGCCGTGTG 395

Qy 186 ACAGGAATTGAGGAGAACAGCCGAACGGCAACTGGCTGTTCGATCGACGATGA 245

Db 396 TGCCCAATTGCGTAAACCTAGCCGTACCGCTACGGCTGTTCTCGAGTTCCC 455

Qy 246 GAGGCCGGTGTAGGGATGAGCTGGCTGACATCGTATCACTCCCGACCA 305

Db 456 GTCGATCCGTCGTCGTCGAGGTGATGGTAGCCGAGGTGGCCGCGCA 515

Qy 306 ACCGACAGCAACACAG 321

Db 516 GCGGGCAAGAAAGAG 531

RESULT 14
ID ABX09144 Standard; DNA; 45190 BP.

XX ABX09144;

XX DT 08-APR-2003 (first entry)

XX DE Mycobacterium tuberculosis H37RV BAC clone BAC-Rv267.

XX KW Mycobacterioses; survival; protective antigen; vaccine; mycobacterial disease; tuberculosis; leprosy; ds; cosmid.

XX OS Mycobacterium tuberculosis.

XX PN WO200274903-A2.

XX

PD 26-SEP-2002.
XX PF 22-FEB-2002; 2002WO-IB001973.

XX PR 22-FEB-2001; 2001US-0270123P.
XX PA (INSP) INST PASTEUR.

XX PI Cole S;
XX Disclosure; Fig 8; 874pp; English.

XX WPI; 2002-759885/82.

XX DR Identifying and selecting genes for survival or virulence of mycobacteria by a comparative genomic analysis of the sequences of Mycobacterium tuberculosis and *M. leprae*.

XX PT Disclosure; Fig 8; 874pp; English.

XX This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polynucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting *M. tuberculosis* or *M. leprae* infection. The method reduces the number of potential new targets and protective antigens for new drugs and vaccine compositions to treat and prevent mycobacterial diseases, particularly tuberculosis and leprosy. The present sequence represents a Mycobacterial cosmid DNA sequence used in the method of the invention

XX Sequence 45190 BP; 7490 A; 14522 C; 15204 G; 7974 T; 0 U; 0 Other;

XX SQ Query Match 12.6%; Score 40.4%; DB 6; Length 45190;
XX Best Local Similarity 50.4%; Pred. No. 2;
XX Matches 129; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

XX Qy 72 TGGGGCAACATGGTGGGGGCCAACGTTCCGTGCGAGAGGGGCCAAACG 131

XX Db 4805 TCGGCTGCAACAGACCGTGGGGAGACTGGCACAGGGTTACCGGACTAACGGTGT 4864

XX Qy 132 GCAGGCCGACATTGAGCTTGAGGCTATCGGGCTGCGGGACATC 185

XX Db 4865 CAATCGAGTCCTGCGCCGGGGAGATCTGGCGGCGGCGGCGGT 4924

XX Qy 186 ACACCAAATGAGGAGAACAGCCGAACGGCAACTGGCTGTTCGATCGCATCTCGAGGGATCTCGAGGGT 245

XX Db 4925 TGCCCAATTGCGTAAACCTAGCCGTACCGTGTACCGGTTACCGGCTTACCGTGTCTCGACTTCCC 4984

XX Qy 246 GCAGGCCGGCTTGGGGAGATCTGGCTGCGGGCGGAGGTGGCCGCGCA 305

XX Db 4985 GTCGATCCGTCGTCGTCGAGGTGATGGTAGCCGAGGTGGCCGAGGA 305

XX Qy 306 ACCCCACAGCAACAG 321

XX Db 5045 GCGGGCAAGAAAGAG 5060

RESULT 15
AAI99682_11

Continuation (12 of 45) of AAI99682 from base 1100001 (Mycobacterium tuberculosis strain LOCUS AAI99682 Accession AAI99682

WP Sequence split into 45 fragments
WP Fragment Name Begin End

WP AAI99682_00 1 110000

WP AAI99682_01 100001 210000

WP AAI99682_02 200001 310000

WP AAI99682_03 300001 410000

WP AAI99682_04 400001 510000

WP AAI99682_05 500001 610000

WP AAI99682_06 600001 710000

WP AAI99682_07 700001 810000

WP AAI99682_08 800001 910000

WP	AAI99682_09	900001	1010000
WP	AAI99682_10	1000001	1110000
WP	AAI99682_11	1100001	1210000
WP	AAI99682_12	1200001	1310000
WP	AAI99682_13	1300001	1410000
WP	AAI99682_14	1400001	1510000
WP	AAI99682_15	1500001	1610000
WP	AAI99682_16	1600001	1710000
WP	AAI99682_17	1700001	1810000
WP	AAI99682_18	1800001	1910000
WP	AAI99682_19	1900001	2010000
WP	AAI99682_20	2000001	2110000
WP	AAI99682_21	2100001	2210000
WP	AAI99682_22	2200001	2310000
WP	AAI99682_23	2300001	2410000
WP	AAI99682_24	2400001	2510000
WP	AAI99682_25	2500001	2610000
WP	AAI99682_26	2600001	2710000
WP	AAI99682_27	2700001	2810000
WP	AAI99682_28	2800001	2910000
WP	AAI99682_29	2900001	3010000
WP	AAI99682_30	3000001	3110000
WP	AAI99682_31	3100001	3210000
WP	AAI99682_32	3200001	3310000
WP	AAI99682_33	3300001	3410000
WP	AAI99682_34	3400001	3510000
WP	AAI99682_35	3500001	3610000
WP	AAI99682_36	3600001	3710000
WP	AAI99682_37	3700001	3810000
WP	AAI99682_38	3800001	3910000
WP	AAI99682_39	3900001	4010000
WP	AAI99682_40	4000001	4110000
WP	AAI99682_41	4100001	4210000
WP	AAI99682_42	4200001	4310000
WP	AAI99682_43	4300001	4410000
WP	AAI99682_44	4400001	4411529

Query Match 12.6%; Score 40.4%; DB 4; Length 110000;
 Best Local Similarity 50.4%; Pred. No. 2..2;
 Matches 129; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

Qy	72	TGCGCGGAACATGGTCCGCCGAGCTGGTCCGCCGAGGATCTGGCACTGGTTACCGGACTAACGGTGT	29484
Db	29425	TGGCTGAAACGACCGTGCGAGCAGTGGCTGAGGTTACGGGACTGGTCAACGGGTTACCGGACTAACGGTGT	
Qy	132	GCAACGCGAACCTCGAGGTATCGGCCGAGCGTGTGGATGATGATGTTGAGTCGACGACATC 185	
Db	29485	CAATCGCGAGCTGGCTCTGGCTCTGGCGAGGATCTGGCGAGGTTGAGTCGACGCGGGTGT 29544	
Qy	186	ACAGGAATCGAGCACACAGCCGAACACTGGGCTGTGGATGATCTGGCACTGGTGT 29604	
Db	29545	TGCCAATCTGCCTACAGTAGCTGGTACGGGTTGAGTCGAGTCCC 29664	
Qy	246	GCAGCGCGCTTGAGGGGGTGAACCTCGGGCTGGCATCGTATACTTCCCGACGA 305	
Db	29605	GTCTCATCGTGTGAGGTTACGGGCTGGCTGCGCAACGGCTGGCCGCA 29664	
Qy	306	ACCGACAGCAACAG 321	
Db	29665	GCGGGCAGCAAGAG 29680	

AF143772	Mycobacte					
AE017231	Mycobacte					
AC129226	Oryza sat					
AK062705	Oryza sat					
AC118132	Oryza sat					
AP005564	Bradyrhiz					
AP005339	Streptomy					
AB096160	Cercopith					
AP046493	Oryza sat					
AP004585	Oryza sat					
AE05681	Caulobact					
AL646076	Ralstonia					
AB017242	Mycobacte					
AE017235	Mycobacte					
CQ462190	Sequence					
AB011659	Xanthomon					
AL939104	Streptomy					
AP005560	Bradyrhiz					
AB016119	Chromobac					
BX572595	Rhodopsel					
AK072093	Oryza sat					
US7682	Rhodobacter					
AC016781	Genomic S					
AC084764	Oryza sat					
RP005037	Streptomy					
AL939106	Streptomy					
20	42.8	13.3	71286	1	AF143772	
21	42.8	13.3	301068	1	AE017231	
22	42.6	13.3	131946	8	AC129226	
23	42.4	13.2	646	8	AK062705	
24	42.4	13.2	168560	8	AC118132	
c	42	13.1	299750	1	AP005564	
c	26	42	13.1	299925	1	AP005339
c	27	41.8	13.0	106873	14	AB096160
c	28	41.8	13.0	147891	8	AP004585
c	29	41.8	13.0	163371	8	AP004585
c	30	41.6	13.0	10507	1	AE005681
c	31	41.4	12.9	216056	1	AL646076
c	32	41.2	12.8	289308	1	AE017242
c	33	41.2	12.8	309267	1	AE017235
c	34	41	12.8	400	6	CQ462190
c	35	41	12.8	10772	1	AB011659
c	36	40.8	12.7	299050	1	SC0939104
c	37	40.8	12.7	300450	1	AP005560
c	38	40.8	12.7	300917	1	AB016119
c	39	40.8	12.7	349260	1	BX572595
c	40	40.6	12.6	4161	8	AK072093
c	41	40.6	12.6	86896	1	RCU57682
c	42	40.6	12.6	151269	8	AC016781
c	43	40.6	12.6	160365	2	AC084764
c	44	40.6	12.6	299425	1	AP005037
c	45	40.6	12.6	314100	1	SC0939106
OM nucleic - nucleic search, using sw model						
Run on:	February 10, 2005, 03:45:06 ; Search time 2015 Seconds (without alignments) 7533.496 Million cell updates/sec					
Title:	US-10-647-089-93					
Perfect score:	321					
Sequance:	1 ttgaccacaaggcaactaa.....acgaaccggacagcaaacag 321					
Scoring table:	IDENTITY_NUC					
	GapOp 10.0 , Gapext 1.0					
Searched:	4526729 seqs, 23644849745 residues					
Total number of hits satisfying chosen parameters:	9053458					
Minimum DB seq length:	0					
Maximum DB seq length:	2000000000					
Post-processing: Minimum Match %						

ALIGNMENTS

RESULT 1		PAT 20-FEB-2004	
AR456084	AR456084	321 bp	DNA
LOCUS	Sequence 93 from patent US 6686166.		
DEFINITION			
ACCESSION	AR456084		
VERSION	AR456084.1		
KEYWORDS	GI:42691080		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 321)		
AUTHORS	Behr, M., Small, P., Schoolnik, G. and Wilson, M.A.		
TITLE	Molecular differences between species of the M. tuberculosis complex		
JOURNAL	US 6686166-A 93 03-FEB-2004;		
FEATURES	Location/Qualifiers		
source	1. .321		
	/organism="Unknown"		
	/mol_type="genomic DNA"		

ORIGIN	Query	Match	100.0%	Score	321;	DB	6;	Length	321;
	Best Local	Similarity	100.0%	Prod.	No.	5..9e-49;			
	Mismatches	0;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	1	TTGACCCCAAGGCCATTAAGCCGATTAAGCCGATTCGGTCCGGCAGGGCTCAAAGCCCCCGT	60						
Db	1	TTGACCCCAAGGCCATTAAGCCGATTCGGTCCGGCAGGGCTCAAAGCCCCCGT	60						
Qy	61	CGGAATTCGGTTGGGGAAACATGGTTGGCCGGCAGCTTCGGCCAGAGGGC	120						
Db	61	CGGAATTCGGTTGGGGAAACATGGTTGGCCGGCAGGGCTCAAAGCCCCCGT	120						
Qy	121	CGGCCCAACGGCGGCCACCTCGAGGGTATCCCGCGAGGTAACTCCGAGATGGTGC	180						
Db	121	CGGCCCAACGGCGGCCACCTCGAGGGTATCCCGCGAGGTAACTCCGAGATGGTGC	180						
Qy	181	ACATCACGAAATTGACGACGAACTCGCCGACTCGCGCTGTTGCCATGCATCTGCAC	240						
Db	181	ACATCACGAAATTGACGACGAACTCGCCGACTCGCGCTGTTGCCATGCATCTGCAC	240						
Qy	241	GATGAGCAAGCGCCGGCTTGGGGGATGAAGCTGGTGGCATCGGTAACTTCCCC	300						

Db 241 GATGAGCAGCCGCTTGGCGGGATGAAGCTGGCATCCATTCACTTCCC 300
 Qy 301 GACCBACCCGACAGAAAG 321
 Db 301 GACGACCCGACAGAAAG 321

RESULT 2
 AX074032 LOCUS AX074032 Sequence 14 from Patent WO0104151. DNA linear PAT 06-FEB-2001
 DEFINITION Sequence 14 from Patent WO0104151.
 ACCESSION AX074032
 VERSION AX074032.1 GI:12710257
 KEYWORDS Mycobacterium tuberculosis
 SOURCE Mycobacterium tuberculosis
 ORGANISM Bacteria; Actinobacteria; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex
 1.
 REFERENCE Andersen, P. and Skjødt, R.
 Tuberculosis vaccine and diagnostics based on the mycobacterium tu
 berculosis esat-6 gene family
 Patent: WO 0104151-A1 14 JAN 2001;
 States Serum Institut (DK)
 Location/Qualifiers
 1..324 /note="unnamed protein product"
 /codon_start=1
 /transl_table=11
 /protein_id="CAC28442.1"
 /db_xref="GI:12710258"
 /translation="MTHKRTKRQPAIAAGINAPRANRVRQHGPADVPSAEQRRAQR
 QRDLEATRAYAVTSHEIDDDTAELLISMHLDEQRLEAGMKLGPHYPHPDE
 PSDSKQ"
 ORIGIN

Query Match Score 321; DB 6; Length 324;
 Best Local Similarity 100.0%; Pred. No. 5.9e-49;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGACCCACAAGGCCACTAAACGCCAGCCAGGCTAACGCCCGCGT 60
 Db 1 TTGACCCACAAGGCCACTAAACGCCAGCCAGGCTAACGCCCGCGT 60

Qy 61 CGGAATTCGGTTCGGCGCAACATGGTTGGCGCCAGTCCGTGGCG 120
 Db 61 CGGAATTCGGTTCGGCGCAACATGGTTGGCGCCAGTCCGTGGCG 120

Qy 121 CGGGCCACAAGGGAAGCGAACCTCGAGCTATCGCCGAGCTAAC 180
 Db 121 CGGGCCACAAGGGAAGCGAACCTCGAGCTATCGCCGAGCTAAC 180

Qy 181 ACATCACAGAAATCGAGCAGCACAGCGAACACTGGCGTGGCATCTCGAC 240
 Db 181 ACATCACAGAAATCGAGCAGCACAGCGAACACTGGCGTGGCATCTCGAC 240

Qy 241 GATGAGCAGCCGGGCTGAGGGGATGAAGCTCGCTGCATCGTAACTTCCC 300
 Db 241 GATGAGCAGCCGGGCTGAGGGGATGAAGCTCGCTGCATCGTAACTTCCC 300

Qy 301 GAGAACCCGACGAAACAG 321
 Db 301 GAGAACCCGACGAAACAG 321

W|COMMENT Sequence split into 44 fragments LOCUS AE000516 Accession AE000516
 Fragment Name Begin End
 AE000516_00 1 110000
 AE000516_01 100001 210000
 AE000516_02 200001 310000
 AE000516_03 300001 410000
 AE000516_04 400001 510000
 AE000516_05 500001 610000
 AE000516_06 600001 710000
 AE000516_07 700001 810000
 AE000516_08 800001 910000
 AE000516_09 900001 1010000
 AE000516_10 1000001 1110000
 AE000516_11 1100001 1210000
 AE000516_12 1200001 1310000
 AE000516_13 1300001 1410000
 AE000516_14 1400001 1510000
 AE000516_15 1500001 1610000
 AE000516_16 1600001 1710000
 AE000516_17 1700001 1810000
 AE000516_18 1800001 1910000
 AE000516_19 1900001 2010000
 AE000516_20 2000001 2110000
 AE000516_21 2100001 2210000
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 AE000516_28 2800001 2910000
 AE000516_29 2900001 3010000
 AE000516_30 3000001 3110000
 AE000516_31 3100001 3210000
 AE000516_32 3200001 3310000
 AE000516_33 3300001 3410000
 AE000516_34 3400001 3510000
 AE000516_35 3500001 3610000
 AE000516_36 3600001 3710000
 AE000516_37 3700001 3810000
 AE000516_38 3800001 3910000
 AE000516_39 3900001 4010000
 AE000516_40 4000001 4110000
 AE000516_41 4100001 4210000
 Continuation [30 of 44] of AE000516 from base 2900001 (AE000516 Mycobacterium tuberculosis)

Query Match Score 321; DB 1; Length 110000;
 Best Local Similarity 100.0%; Pred. No. 2.e-49;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGACCCACAAGGCCACTAAGGCCAGCCAGGCTAACGCCCGCGT 60
 Db 71695 TTGACCCACAAGGCCACTAAGGCCAGCCAGCTAAC 4300000 4403837

Qy 61 CGGAATTCGGTTCGGCGCAACATGGTTGGCGCCAGTCCGTGGCG 120
 Db 71635 CGGAATTCGGTTCGGCGCAACATGGTTGGCGCCAGCTGGCG 120

Qy 121 CGGGCCACAAGGGAAGCGAACCTCGAGCTATCGCCGAGCTAAC 180
 Db 71695 TTGACCCACAAGGCCAGCCAGCTAAC 4300000 4403837

Qy 61 CGGAATTCGGTTCGGCGCAACATGGTTGGCGCCAGTCCGTGGCG 120
 Db 71635 CGGAATTCGGTTCGGCGCAACATGGTTGGCGCCAGCTGGCG 120

Qy 121 CGGGCCACAAGGGAAGCGAACCTCGAGCTATCGCCGAGCTAAC 180
 Db 71695 TTGACCCACAAGGCCAGCCAGCTAAC 4300000 4403837

Qy 61 CGGAATTCGGTTCGGCGCAACATGGTTGGCGCCAGTCCGTGGCG 120
 Db 71635 CGGAATTCGGTTCGGCGCAACATGGTTGGCGCCAGCTGGCG 120

Qy 121 CGGGCCACAAGGGAAGCGAACCTCGAGCTATCGCCGAGCTAAC 180
 Db 71695 TTGACCCACAAGGCCAGCCAGCTAAC 4300000 4403837

Qy 181 ACATCACAGAAATCGAGCAGCACAGCGAACACTGGCGTGGCATCTCGAC 240
 Db 181 ACATCACAGAAATCGAGCAGCACAGCGAACACTGGCGTGGCATCTCGAC 240

Qy 241 GATGAGCAGCCGGGCTGAGGGGATGAAGCTCGCTGCATCGTAACTTCCC 300
 Db 241 GATGAGCAGCCGGGCTGAGGGGATGAAGCTCGCTGCATCGTAACTTCCC 300

Qy 301 GAGAACCCGACGAAACAG 321
 Db 301 GAGAACCCGACGAAACAG 321

RESULT 3
 AE000516_29/c

Qy	301	GACGAACCCGACAGCAAACAG	321	(128 aa), PASTA scores: opt: 767, E(): 4e-47, (88.1% identity in 126 aa overlap); Q9X/B3 MUCB16 0.14c PUTATIVE GLOBIN from Mycobacterium leprae (131 aa); Q9J250 SCGD10_14c PUTATIVE GLOBIN from Streptomyces coelicolor (137 aa), PASTA scores: opt: 466, E(): 5.7e-26, (53.6% identity in 125 aa overlap). Also similar to 031607 YJBI PROTEIN from Bacillus subtilis (132 aa), PASTA scores: opt: 294, E(): 6.6e-14; (39.85% identity in 128 aa overlap). COULD BELONG TO PHOTOTOZAN/CYANOBACTERIAL GLOBIN FAMILY PROTEIN."
Db	71395	GACGAACCCGACAGCAAACAG	71375	
RESULT 4				
BX842580/C	BX842580	346051 bp	DNA linear	BCT 1.0-JUN-2004
LOCUS				
DEFINITION				Mycobacterium tuberculosis H37Rv complete genome; segment 9/13.
ACCESSION				AL008687 AL00967 AL021185 AL021286 AL123456
Z77250	Z77254	280225	283863	295556 296072 297051 298045
298309				
VERSTON				
KEYWORDS				
SOURCE				
ORGANISM				
				Mycobacterium tuberculosis H37Rv
				Actinomycetales; Actinomycetes; Mycobacterium; Mycobacteriaceae; Mycobacteriae; Mycobacterium tuberculosis complex.
REFERENCE				
AUTHORS	Cole,S.T., Brosch,R., Parkhill,J., Garnier,T., Churcher,C., Harris,D., Gordon,S.V., Eiglmeier,K., Gas,S., Barry III,C.E., Tekaia,F., Badcock,K., Basham,D., Chillingworth,T., Connor,F., Davies,R., Devlin,K., Feltwell,T., Gentles,S., Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J., Moulou,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A., Rajandream,M.A., Rogers,J., Rutte,S., Seeger,K., Steilton,S., Squares,S., Squires,R., Sulston,J.E., Taylor,K., Whitehead,S. and Barrell,B.G.			
TITLE	Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence			
JOURNAL	Microbiology (Reading, Engl.)	148 (Pt 10)	2967-2973	(2002)
MEDLINE	9685393	937-544		
PUBMED	98285987			
REFERENCE	2			
AUTHORS	Camus,J.C., Pryor,M.J., Medigue,C. and Cole,S.T.			
TITLE	Re-annotation of the genome sequence of Mycobacterium tuberculosis H37Rv			
JOURNAL	Microbiology (Reading, Engl.)	148 (Pt 10)	2967-2973	(2002)
MEDLINE	98285987			
PUBMED	9364230			
REFERENCE	3			
AUTHORS	Parhail,J.	(bases 1 to 346051)		
JOURNAL	Direct Submission			
TITLE	Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unité de Génétique Moléculaire Bactérienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk			
COMMENT	On or before Jan 28, 2004 this sequence version replaced gi:3261504, gi:3261505, gi:3261507, gi:3261617, gi:3261620, gi:3261625, gi:3261685, gi:3261776, gi:3261783, gi:3261793, gi:3261840, gi:3261838.			
Notes:				
				Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/).
FEATURES	source			
	1.	346051		
				Location/Qualifiers
				1. organism="Mycobacterium tuberculosis H37Rv"
				/mol type="Genomic DNA"
				/strain="37Rv"
				/db_xref="taxon:833322"
				142. .528
				gene="gibob"
				/locus tag="Rv2472"
				142. .528
				gene="gibob"
				/locus tag="Rv2470"
				139. E(): 0.01, (45.35% identity in 75 aa overlap).
				/function="OXYGEN CARRIER, INVOLVED IN OXYGEN TRANSPORT."
				/note="Rv2470, (MTV008 26), len: 128 aa. Possible globin, globin-like protein, highly similar to Q9CC9 Gu0 ML1253 HEMOGLOBIN-LIKE (OXYGEN CARRIER) from Mycobacterium leprae
				/evidence=experimental
				/transl_table=11

/product="CONSERVED HYPOTHETICAL PROTEIN"
 /protein_id="CAA16049_1"
 /db_xref="GI:2791512"
 /translation="MMRIIAVFLPGEVITFVSESVIRSPRAAVLRAASDAA
 ILTATPEPNHLDALAGQAKLAPTSIDAAHPARPARDPCLYPTRQALPTG"
 25312 . 3248
 /locus_tag="Rv2473"
 /locus_tag="Rv2473"
 /function="UNKNOWN"
 /note="Rv2473, (MTV008.29), len: 238 aa. Possible
 pro-alanine-rich membrane protein, with possible
 transmembrane domain around aa 81-104."
 /codon_start=1
 /transl_table=11
 /product="POSSIBLE ALANINE AND PROLINE RICH MEMBRANE
 PROTEIN"
 /protein_id="CAA16050_1"
 /db_xref="GI:2791513"
 /translation="MAPISSVYASLELLMPWPSAAASCVGWRRTTATASORYHRPMNSDT
 PFAPEPYEORPVGVPGRWDGSSRSRSPSPTSPSPRWSVIALAIVAVSIYGVVG
 PRDOPDKPSPLSPSAPFTPSQISDAKENVCPAHLRVQAWLNTNQANPVPGDPTGD
 LAVLAANRRLAISGGDTYLRLRITAEPATPAELRDAVRSLANALQELAVNTLGAQDSV
 complement(1280 . 3933)
 /locus_tag="Rv2474C"
 complement(3280 . 3931)
 /locus_tag="Rv2474C"
 /function="UNKNOWN"
 /note="Rv2474C, (MTV008.30c), len: 217 aa. Hypothetical
 protein. Shows weak similarity with Q9L246|SC6D10.18C
 HYPOTHETICAL 24.9 kDa PROTEIN from Streptomyces coelicolor
 (238 aa). FASTA score: opt: 111, E(): 5.6, (30% identity
 in 233 aa overlap) BLASTP scores: Score= 135, E= 3.5e-07,
 P= 3.5e-07, Identities= 55/182 (30%)."
 /codon_start=1
 /transl_table=11
 /product="CONSERVED HYPOTHETICAL PROTEIN"
 /protein_id="CAA16051_1"
 /db_xref="GI:2791514"
 complement(1939 . 4355)
 /locus_tag="Rv2475C"
 /function="UNKNOWN"
 /note="Rv2475C, (MTV008.31c), len: 138 aa. Conserved
 hypothetical protein, showing similarity with
 Q9L245|SC6D10.19C HYPOTHETICAL 19.2 kDa PROTEIN from
 Streptomyces coelicolor (136 aa). FASTA scores: opt: 236,
 E(): 1.9e-09, (34.1% identity in 126 aa overlap). Also
 some similarity with AA4K4393|Z97050|MTC18.3 CONSERVED
 HYPOTHETICAL PROTEIN from Mycobacterium tuberculosis
 cosmid I (151 aa). FASTA scores: opt: 147, E(): 0.00025,
 (29.2% identity in 120 aa overlap)."
 /codon_start=1
 /transl_table=11
 /product="CONSERVED HYPOTHETICAL PROTEIN"
 100.0% Score 321; DB 1; Length 346051;
 Best Local Similarity 100.0%; Pred. No. 1.8e-19;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query 1 TTGACCCAGGCCACTAACGCCAGCACTGGCGGTCAACCCCGCT 60
 Db 203873 TTGACCCAGGCCACTAACGCCAGCACTGGCGGTCAACCCCGCT 203814
 Query 61 CGGAATCGGTTEGGGGCAACATGGTGGCCGGCCAGTGGCTCGCCAGACGCC 120
 Db 203813 CGGAATCGGTTEGGGGCAACATGGTGGCCGGCCAGTGGCTCGCCAGACGCC 203754

Query Match 121 CGGCCCCAACGGGAGCCCTGAGCTATCGGGAGCTACGCCAGATGGTGGCG 180
 Best Local Similarity 100.0%; Pred. No. 1.8e-19;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query 181 ACATCACCGAAATCGGAGCAACGCCAGCACTGGCGGTCAACCCCGCT 60
 Db 203753 CGGCCCCAACGGGAGCCCTGAGCTATCGGGAGCTACGCCAGATGGTGGCG 203694
 Query 181 ACATCACCGAAATCGGAGCAACGCCAGCACTGGCGGTCAACCCCGCT 240
 Db 203693 ACATCACCGAAATCGGAGCAACGCCAGCACTGGCGGTCAACCCCGCT 203634
 Query 241 GATGAGCAAGCGCCGTTGAGCTGGCATCGGTATCGTGGCTGGCTGGCG 300
 Db 203633 GATGAGCAAGCGCCGTTGAGCTGGCATCGGTATCGTGGCTGGCG 203574
 Query 301 GACGAACCAGAACAG 321
 Db 203573 GACGAACCAGAACAG 203553

RESULT 5
 MSGY223 42061 bp DNA linear sequence from clone y223.
 LOCUS MSGY223
 DEFINITION Mycobacterium tuberculosis sequence from clone y223.
 VERSION AD000019.1 GI:17117737
 KEYWORDS Mycobacterium tuberculosis
 SOURCE ORGANISM Mycobacterium tuberculosis
 AUTHORS Bacteria; Actinobacteria; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium
 tuberculosis complex.
 REFERENCE 1 (bases 1 to 42061)
 TITLE Direct Submission
 JOURNAL Submitted (11-OCT-1996) L.D., Genome Therapeutics Corporation, 100
 Beaver Street, Waltham, MA, USA, 02154 du@cric.com
 COMMENT GSDB:S:1004712.
 FEATURES Location/Qualifiers
 source 1 . 42061
 /organism="Mycobacterium tuberculosis"
 /mol_type="genomic DNA"
 /db_xref="taxon:1773"
 /clone="y223"
 ORIGIN

Query Match 96.1% Score 309; DB 1; Length 42061;
 Best Local Similarity 99.7%; Pred. No. 4e-47;
 Matches 320; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 1 TTGACCCAGGCCACTAACGCCAGCACTGGCGGTCAACCCCGCT 60
 Db 5783 TTGACCCAGGCCACTAACGCCAGCACTGGCGGTCAACCCCGCT 5842
 Query Match 61 CGGAATCGGTGGGGCAACATGGTGGCGGAGCTTCGGTCCGGAGCGCG 120
 Db 5843 CGGAATCGGTGGGGCAACATGGTGGCGGAGCTTCGGTCCGGAGCGCG 5902
 Query Match 121 CGGCCCCAACGGGAGCCAGCACTGGCGGTCAACCCCGCT 180
 Db 5903 CGGCCCCAACGGGAGCCAGCACTGGCGGTCAACCCCGCT 5962
 Query Match 181 ACATCACCGAAATCGGAGCAACGCCAGCACTGGCGGTCAACCCCGCT 240
 Db 5963 ACATCACCGAAATCGGAGCAACGCCAGCACTGGCGGTCAACCCCGCT 6022
 Query Match 241 GATGAGCAAGCGCCGTTGAGCTGGCATCGGTATCGTGGCTGGCG 300
 Db 6023 GATGAGCAAGCGCCGTTGAGCTGGCATCGGTATCGTGGCTGGCG 6081
 Query Match 301 GACGAACCAGAACAG 321
 Db 6082 GACGAACCAGAACAG 6102

Qy	66	TGGCGTTGGCGGAAACATGGTGGCCGAGCTCCGGAGAGGCCGCC 125	gene	1094. .4009
Db	35020	CCTCGGGCGGAAACAGCGGTACGCCGATCAGGCCGAGCTGCCTC 34961	CDS	1094. .4009
Qy	126	CCAACGGCAGGGGACTCAAGGTATCCCGAGCTAGCCGAGTGTCATC 185	/gene="tnpA"	/gene="tnpA"
Db	34960	CGACCTGGAGGGGGAAACAGGGGACCGGCCCTCAGGCCAGCG 34901	/function="transposition"	/function="transposition"
Qy	186	ACACGAATGCGACGACAGCGGAATGGCGTGTTCGATCGACATCGATCA 245	/codon_start=1	/codon_start=1
Db	34900	GAAGGCCACGGAGGGCCCGGCCGACAGGTGGCGGAGCTGGTAAGGT 34841	evidence=experimental	evidence=experimental
Qy	246	GCAGGGCGCTTGAGGGGGATGAAGCTGGCTGGCATCG 288	/transl_table=11	/transl_table=11
Db	34840	GCAGGCCAACCGCCAGGCCAGGCCACAGGACAG 34798	/product="transposase"	/product="transposase"
RESULT 8				
AB063332/C	AB063332	67056 bp DNA circular BCT 16-JUL-2004	gene	1094. .4009
LOCUS	AB063332	Deltiota acidovorans plasmid pUO1. DNA, complete sequence.	CDS	1094. .4009
DEFINITION			/gene="tnpA"	/gene="tnpA"
ACCESSION	AB063332		/function="transposition"	/function="transposition"
VERSION	AB063332.1		/codon_start=1	/codon_start=1
KEYWORDS			/evidence=experimental	/evidence=experimental
SOURCE			/product="haloacetate dehalogenase H-2"	/product="haloacetate dehalogenase H-2"
ORGANISM		Deltiota acidovorans	/protein_id="BAC81974.1"	/protein_id="BAC81974.1"
		Deltiota acidovorans Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;	/db_xref="GI:34013301"	/db_xref="GI:34013301"
		Comamonadaceae; Deltiota.	/transl_table=11	/transl_table=11
REFERENCE	1	Sota,M., Endo,M., Nitta,K., Kawasaki,H. and Tsuda,M.	/product="haloacetate dehalogenase H-2"	/product="haloacetate dehalogenase H-2"
AUTHORS		Characterization of a class II defective transposon carrying two	/protein_id="BAC81974.1"	/protein_id="BAC81974.1"
TITLE		haloacetate dehalogenase genes from Deltiota acidovorans plasmid pUO1.	/gene="dehh2"	/gene="dehh2"
JOURNAL	Appl. Environ. Microbiol.	68 (5), 2307-2315 (2002)	/function="dehalogenation"	/function="dehalogenation"
MEDLINE	21972280		/codon_start=1	/codon_start=1
PUBMED	11976102		/evidence=experimental	/evidence=experimental
REFERENCE	2	Sota,M., Kawasaki,H. and Tsuda,M.	/product="haloacetate dehalogenase H-2"	/product="haloacetate dehalogenase H-2"
AUTHORS		Structure of haloacetate-catabolic IncP-1beta plasmid pUO1 and	/protein_id="BAC81974.1"	/protein_id="BAC81974.1"
TITLE		genetic mobility of its residing haloacetate-catabolic transposon	/db_xref="GI:34013301"	/db_xref="GI:34013301"
JOURNAL	J. Bacteriol.	185 (22), 6741-6745 (2003)	/transl_table=11	/transl_table=11
MEDLINE	12457023		/protein_id="BAC81975.1"	/protein_id="BAC81975.1"
PUBMED	14594853		/db_xref="GI:34013302"	/db_xref="GI:34013302"
REFERENCE	3	(bases 1 to 67066)	/transl_table=11	/transl_table=11
AUTHORS	Sota,M., Tsuda,M. and Kawasaki,H.		/product="MSPEBKIVHEKSAQDFDSOSMSYGDYLHDEMLKAQHPLPAHD	/product="MSPEBKIVHEKSAQDFDSOSMSYGDYLHDEMLKAQHPLPAHD
TITLE	Direct Submission		/EMFOHQTSLEWMKLMJHELMMAATRIBATEBOLDAFKMLARUSRMEQLCWAWRV	/EMFOHQTSLEWMKLMJHELMMAATRIBATEBOLDAFKMLARUSRMEQLCWAWRV
JOURNAL	Submitted	(19-JUN-2001) Masahiro Sota, Institute for Environmental	/RTSLSYDRAILARRGLAAPPSSYVN"	/RTSLSYDRAILARRGLAAPPSSYVN"
MEDLINE	12457023	Sciences, Department of Environmental Simulation; I-7 Ienoma,		
PUBMED	14594853	Ouchi, Rokkasho, Aomori 039-3212, Japan (E-mail:sota@ies.or.jp.		
FEATURES		Tei:81-175-21-1407, Fax:91-175-71-1401)		
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repeat_region	note="IS1071"			

Query Match 14.4%; Score 46.2; DB 1; Length 67066;
 Best Local Similarity 47.7%; Pred. No. 33; Mismatches 0; Gaps 0;
 Matches 135; Conservative 0; Missmatches 148; Indels 0;

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Qy	66	TGCGTTGGGCCACATGGTGGCGGAGCTTCGTGCGAGCAGGGCGCC	125
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Qy	126	CCAAGCCAGGCCAGCTTGCGCTAACGGCTAACCGCTAACCGCTAACCG	185
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Qy	186	ACAGGAATTCGAGCACACCCGAGCTTGCGCATGATCTCAGCATGTA	245
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Qy	246	GCAGCGCGGTGAGGGGATGAAGCTGCGCTGGATCG	288
Db	60078	GCGGCCAGGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAG	60036

RESULTS 9

	AY365053/c	AY365053	8768B bp	DNA	circular BCT 04-JUN-2004
LOCUS	Wautersia eutropha	strain JMp134	plasmid	pJp4	, complete sequence.
DEFINITION					
ACCESSION	AY365053	AY365053			
VERSION	AY365053.1	GI:39777443			
KEYWORDS					
SOURCE	Wautersia eutropha				
ORGANISM	Wautersia eutropha				
BACTERIA	Proteobacteria	Beta-proteobacteria	Burkholderiales	Burkholderiaceae	
BURKHOLDERIA					
REFERENCE	1	(bases 1 to 8768B)			
AUTHORS	Trefault,N., De la Iglesia,R., Molina,A.M., Manzano,M., Ledger,T., Perez-Pantoja,D., Sanchez,M.A., Stuardo,M. and Gonzales,B.				
TITLE	Genetic organization of the catabolic plasmid pJp4 from Ralstonia eutropha JMp134 (pJp4) reveals mechanisms of adaptation to chloroaromatic pollutants and evolution of specialized pathways				
JOURNAL	Environ. Microbiol.	6 (7), 655-668	(2004)		
REFERENCE	2	(bases 1 to 8768B)			
AUTHORS	Trefault,N. and Gonzalez,B.				
TITLE	Direct Submission				
JOURNAL	Submitted (11-AUG-2003) Departamento de Genetica Molecular Y Microbiologia, Facultad de Ciencias Biologicas, Pontificia Universidad Catolica de Chile, Casilla 114-D, Santiago, Chile				
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Query Match 14.4%; Score 45.2; DB 1; Length 8768;
 Best Local Similarity 47.4%; Pred. No. 31; Indels 0; Gaps 0;
 Matches 135; Conservative 0; Mismatches 148;

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Db	1848 CGACAGGCCAGAGGCCAACGGCAGACGGCTGAGGGCTGGCGA 1789
Qy	66 TCGGTTGGGGAAACATGGTGGCCGCCAGCTTCGTCGCCAGGCCGC 125
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Qy	126 CCACGGCCGGCAGCTGGGTATCCGGCAGCTAACGGCTAACGGCATC 185
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Qy	186 ACAGAAATCGACGAGCACAGCAGCAACTGGCGCTGTGCGATCTGAGATGA 245
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 VERSION U66917_2 GI:13937422
 SOURCE Pseudomonas sp. ADP
 ORGANISM Pseudomonas sp. ADP
 Bacteria; Proteobacteria.
 (bases 34964 to 36388)
 de Souza, M.L., Wackett, L.P., Boundy-Mills, K.L., Mandelbaum, R.T. and Sadowsky, M.J.

TITLE Cloning, characterization, and expression of a gene region from *Pseudomonas* sp. strain ADP involved in the dechlorination of atrazine
 Appl. Environ. Microbiol. 61 (9), 3373-3378 (1995)

JOURNAL J. Bacteriol. 180 (1), 152-158 (1998)
 MEDLINE 98083068
 PUBMED 9055410
 REFERENCE 2 (bases 43552 to 46212)
 AUTHORS Boundy-Mills, K.L., de Souza, M.L., Mandelbaum, R.T., Wackett, L.P. and Sadowsky, M.J.
 TITLE The *atzB* gene of *Pseudomonas* sp. strain ADP encodes the second enzyme of a novel atrazine degradation pathway
 JOURNAL J. Bacteriol. 180 (1), 152-158 (1998)
 MEDLINE 98083068
 PUBMED 9422615
 REFERENCE 4 (bases 43552 to 46212)
 AUTHORS Boundy-Mills, K.L., de Souza, M.L., Mandelbaum, R.T., Wackett, L.P. and Sadowsky, M.J.

TITLE Direct Submission (15-AUG-1996) Soil, Water, and Climate, University of Minnesota, 1991 Upper Buford Circle, 439 Borlaug Hall, St. Paul, MN 55108, USA
 REFERENCE 5 (bases 69775 to 71867)
 AUTHORS Sadowsky, M.J., Tong, Z., de Souza, M.L. and Wackett, L.P.
 TITLE Direct Submission (05-AUG-1997) Soil, Water, and Climate Dept., University of Minnesota, 1991 Upper Buford Circle, 439 Borlaug Hall, St. Paul, MN 55108, USA
 REFERENCE 6 (bases 1 to 108845)
 AUTHORS Martinez, B.M., Tomkins, J., Wackett, L.P., Wing, R. and Sadowsky, M.J.
 TITLE Direct Submission (23-JAN-2001) Biochemistry, Molecular Biology and Biophysics, University of Minnesota, 1479 Gortner Ave., 140 Gortner Labs, Saint Paul, MN 55108, USA
 REMARK Nucleotide sequence updated by submitter
 On or before May 3, 2001 this sequence version replaced gi:2736100, gi:173205.

FEATURES Location/Qualifiers
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Best Local Similarity 47.4%; Pred. No. 30;
Matches 135; Conservative 0; Mismatches 148; Indels 0; Gaps 0;
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complete genome.
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VERSION AE016925
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1 (bases 1 to 301457)
REFERENCE 2 (bases 1 to 301457)
AUTHORS Brazilian National Genome Project Consortium
CONSRNM The complete genome sequence of Chromobacterium violaceum reveals
TITLE remarkable and exploitable bacterial adaptability
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (20), 11660-11665 (2003)
MEDLINE 22882880
PUBMED 14500762
REFERENCE 2 (bases 1 to 301457)
AUTHORS Vasconcelos,A.T.R., de Almeida,D.F., Almeida,R., Goncalves,F.C., de
Almeida,L.G.P., de Almeida,R., Andrade,B.M.,
Antonio,R.V., Araripe,J., de Araujo,M.F.F., Filho,S.A., Azevedo,V.,
Batista,A.J., Batista,L.A.M., Batista,J.S., Belo,A., Vander Berg,C.,
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Carneiro,N.P., Carrasco,D.M., Carvalho,C.M.B., Gascardo,J.C.M.,
Cavada,B.S., Chueire,L.M.O., Pasa,T.B.C., Duran,N., Fagundes,N.,

	Palcao, C.L., Pantinatti, F., Farias, J.P., Felipe, M.S.S., Ferrari, L.P., Ferro, J.A., Ferro, M.I.T., Franco, G.R., Gazzani, E.A., Freitas, N.S.A., Furlan, L.R., Gazzanelli, R.T., Gazzani, E.A., Grattapaglia, D., Grisard, E.C., Guimaraes, P.R., Grangeiro, T.B., Grattapaglia, D., Grisard, E.C., Guimaraes, C.T., Hauna, E.S., Hungria, M., Jardim, S.N., Laurino, J., Leo, L.C.T., Passarelli, L., Lima, A., Loureiro, M.F., Lyra, M.C.P., Macedo, M., Madeira, H.M.F., Manfio, G.P., Maranhao, A.Q., Martins, W.S., di Mauro, S.M.Z., de Medeiros, S.R.B., Meissner, R.V., Menck, C.F.M., Moreira, M.A.M., Oliveira, F.F., Nicolas, M.F., Oliveira, J.G., Oliveira, S.C., Paixao, R.F.C., Parente, J.A., Pedrosa, F.O., Pena, S.J.D., Perreira, J.O., Perreira, M., Pedroso, L.S.R.C., Pinto, L.S., Porto, J.R., Portilho, D.P., Neto, C.E.R., Reis, A.M.M., Rigo, L.U., Rondinelli, E., dos Santos, E.B.P., Santos, F.R., Schneider, M.P.C., Seuanez, H.N., Silva, D.W., da Silva, A.L.C., Silva, D.W., Silva, R., Simoes, I.C., Simon, D., Soares, C.M.A., Soares, R.B.A., Souza, E.M., Souza, K.R.L., Souza, R.C., Steffens, M.B.R., Steindel, M., Teixeira, S.R., Urmenyi, T., Vettore, A., Wasserm, R., Zaha, A., and Simpson, A.J.G.	JOURNAL Submitted (22-JAN-2003) Labinfo, LNCC - Laboratorio Nacional de Computacao Cientifica, Rua Getulio Vargas 333, Petropolis, RJ 25651070, Brazil	gene CDS	3010. .3330 /locus_tag="CV3928" /locus_start=3010 /locus_end=3330 /locus_tag="CV3928" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="AQ061599.1" /db_xref="GI:34105234" /translation="MKYNGHGPSPGRFDEBDLPHLMVTSRDNAAFTQWRYWDAPYPEVKRPHIAFEVEDIAQALEGHKLLIAFPNSPPLTVAIEVNQGAPVEMQYDKNN"	
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Query	Match	Score	DB	Length
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	Mismatches	97;	Indels	0;
			Caps	0;
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Db	185515	AGGGCAGCCACCCGCGCCACCGCGCTGGCCACCGCGCTGGCCGCCACCA	185514	
Qy	102	TCCGTGCGCCAGCAGCCCGCCAGCCAGCCAGCTCTGGCAGCTATCCGGCAGGC	161	
Db	185575	CCGGCCGCGCCAGCAGCCAGCCGGCCAGCCGGCCAGCAGCAGCATCGCCGCC	185534	
Qy	162	GTAACCGAGTGGCGACATCACAGAATCTGGAGACACAGCAGCAGACTGGGCT	221	
Db	185635	ACCCCAAGACCCGGGTGGCGAGAGGAGCTGGCCACCCGGCCACCGCCGCCA	185694	
Qy	222	GTTGTCGATGCACTCTGAGC	241	
Db	185695	GTTGCGCGCGAGATCGAG	185714	

RESULTS

RESULT 13
LOCUS AE012255
DEFINITION Xanthomonas campestris str. ATCC 33913
ORGANISM Xanthomonas campestris str. ATCC 33913
VERSION AE012255 AE008922
KEYWORDS Xanthomonas campestris pv. campestris str. ATCC 33913
SOURCE Xanthomonas campestris pv. campestris str. ATCC 33913
Xanthomonadaceae; Xanthomonas.
REFERENCE 1 (bases 1 to 12261)
AUTHORS Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R.,
Quadio,R.B., Monteiro-Vitorelo,C.B., Van Sluys,M.A., Almeida
Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertollo,M.C.,
Camargo,L.E.A., Canarotte,G., Camauan,F., Cardozo,J.,
Chambergo,F., Ciapina,L.P., Cicarelli,R.M.B., Coutinho,L.L.,
Cursino-Santos,J.R., El-Dorry,H., Faria,J.B., Ferreira,A.J.S.,

			ORGANISM	Oryza sativa (japonica cultivar-group)
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
			Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
			Ehrhartoideae; Oryzeae; Oryza.	
	REFERENCE	1	(bases 1 to 10289)	
	AUTHORS	Choisne, N., Orjeda, G., Cattolico, L., Demange, N., Wincker, P., Segurens, B., Pelleier, B., Scarpetti, C., Salanoubat, M., Weissbach, J. and Quétier, F.		
	TITLE	Oryza sativa chromosome 12 sequencing		
	JOURNAL	Unpublished		
	REFERENCE	2 (bases 1 to 104289)		
	AUTHORS	Genoscope.		
	TITLE	Direct Submission		
	JOURNAL	Submitted (21-JUL-2004) Genoscope - Centre National de Séquençage BP 191 91006 EVRY Cedex - FRANCE (E-mail : segrf@genoscope.cns.fr)		
		- Web : www.genoscope.cns.fr)		
	COMMENT	On Jul 21, 2004 this sequence version replaced gi : 50399590.		
		Center: Genoscope / Centre National de Séquençage		
		Center code: GS		
		Web site: http://www.genoscope.cns.fr/		
		Contact: Seqrif@genoscope.cns.fr		
		The following sequence is oriented from the T7 to the SP6 end.		
		Upstream BAC (overlapping the T7 end) : OSJNBA018L16 (AC-BX255875)		
		Downstream BAC (overlapping the SP6 end) : OJ1536_D01 (AC-AL731752)		

		FINISHED SEGMENT STARTS AT BASE 1		
		FINISHED SEGMENT ENDS AT BASE 104289		

	FEATURES	Location/Qualifiers		
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		Best Local Similarity 48.8% ; Pred. No. 93 ;		
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		Query Match Score 44.2 ; DB 8 ; Length 104289;		
		Best Local Similarity 50.2% ; Pred. No. 70 ;		
		Matches 109; Conservative 0; Mismatches 108; Indels 0; Gaps 0;		

		Qy 82 CATGGTCTGCCGGCGACTCCGCTCAAGCCAGGGCTCGGAATCCGTTGGCCAA 81		
		Db 7248 CTCAAGCAGTGATCCATGCCGAGCATGGCATGATTCGGCCANGAA 7307		
		Qy 82 CATGGTCTGCCGGCGACTCCGCTCAAGCCAGGGCTCGGAATCCGTTGGCCAA 141		
		Db 7308 AATGCCCAAGTGCCGGCTGGCGAGGCCATCTGGTCCGGAC 7367		
		Qy 142 CTGGAGGTATGCCGGAGCTGGCTGGCGTGGCGATCGAACATCGAAC 201		
		Db 7368 CTGGAGACTGCCGGCAACGGCTGGTGTGGCAACCCGGCTGGCGGC 7427		
		Qy 202 GACAAGCGGAACTGGCGCTGTGTGATCTCACGAGTGGCGCTGGTGA 261		
		Db 7428 CTGGCCGCCAGCGGGCTGTATGCCAACCTGGCACACCTGGCGCTGGCCG 7487		
		Qy 262 GCGGG 267		
		Db 7488 CAGTGG 7493		

		RESULT 14		
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	LOCUS	CNS08C7V CNS08C7V linear PLN 22-JUN-2004		
	DEFINITION	Oryza sativa chromosome 12. BAC OSJNBA039X19 of library OSJNBA from chromosome 12 of cultivar Nipponbare of sp. japonica of Oryza sativa (rice), complete sequence.		
	ACCESSION	AL731746		
	VERSION	AL731746.5		
	KEYWORDS	HTG.		
	SOURCE	Oryza sativa (japonica cultivar-group)		

		RESULT 15		
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		Sequence split into 18 fragments		
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		LMFLCHR34_01 100001 210000		
		LMFLCHR34_02 200001 310000		
		LMFLCHR34_03 300001 410000		
		LMFLCHR34_04 400001 510000		

Qy	LMFLCHR34_05	500001	610000
	LMFLCHR34_06	600001	710000
	LMFLCHR34_07	700001	810000
	LMFLCHR34_08	800001	910000
	LMFLCHR34_09	900001	1010000
	LMFLCHR34_10	1000001	1110000
	LMFLCHR34_11	1100001	1210000
	LMFLCHR34_12	1200001	1310000
	LMFLCHR34_13	1300001	1410000
	LMFLCHR34_14	1400001	1510000
	LMFLCHR34_15	1500001	1610000
	LMFLCHR34_16	1600001	1710000
	LMFLCHR34_17	1700001	1720777

Continuation (11 of 18) of LMFLCHR34 from base 1000001 (AL499623 Leishmania major chromosome)

Query Match	Score 13.8%	Score 44.2%	DB 2;	Length 110000;
Best Local Similarity	54.7%	Pred. No. 69;		
Matches 88;	Conservative 0;	Mismatches 73;	Indels 0;	Gaps 0;
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Db	15456 GAGCAAGCGCATGCAAGCTGAGCCGCTGCTGCCTGCGCTGGCGGTGCGG	15397		
Qy	172 ATGGTGGGAGATCACAGAAATTCGAGAACAGCGGAAACTGGCGTGTGCGATG	231		
Db	15396 ATGGAGCTCATCTCGAACGAGATCGAGCCAGTTGAGTCAGGAAAGATCAAGTCATCAG	15337		
Qy	232 CATCTGACCATGAGCAAGCGCGCTTGAGCGCCGATGAA	272		
Db	15336 GACCTGCACTTCGAGATGCGCGACTGGAGAAGCTGAA	15296		

Search completed: February 10, 2005, 06:08:07

Job time : 2027 secs

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